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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Computer 154
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Copyright (c) 1993 - 2003 Compugen Ltd.	OM nucleic - nucleic search, using sw model	<pre>Run on: January 22, 2003, 19:04:17 ; Search time 4194.54 Seconds (without alignments) 10726.543 Million cell updates/sec</pre>	cttc 1546	1	Searched: 2054640 segs, 14551402878 residues	To number of hits satisfying chosen parameters: 4109280	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	***  ***  ***  ***  ***  ***  ***  ***  ***  ***  ***  ***  **  ***  ***  ***  ***  ***  ***  ***  ***  ***  ***  ***  ***  **  ***  ***  ***  ***  ***  ***  ***  ***  ***  ***  ***  ***  **  ***  ***  ***  ***  ***  ***  ***  ***  ***  ***  ***  ***  **  ***  ***  ***  ***  ***  ***  ***  ***  ***  ***  ***  ***  **  ***  ***  ***  ***  ***  ***  ***  ***  ***  ***  ***  ***  **  ***  ***  ***  ***  ***  ***  ***  ***  ***  ***  ***  ***  **  ***  ***  ***  ***  ***  ***  ***  ***  ***  ***  ***  ***  **  ***  ***  ***  ***  ***  ***  ***  ***  ***  ***  ***  ***  **  ***  ***  **	
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AX403085 LOCUS DEFINITION ACCESSION VERSION KEYWORDS	SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL

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PRI 18-MAY-2000 Lin,W.-C.
Direct Submission
Submitted (17-MAY-1999) Institute of Biomedical Sciences, Academia Sunica, No. 128, Sec. II, Academia Road, Taipei 115, Taiwan Location/Qualifiers Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarthini, Hominidae, Homo.
1 (bases I to 1556)
Lai.C.H., Chou, C.Y., Ch'ang, L.Y., Liu, C.S. and Lin, W.
Identification of novel human genes evolutionarily conserved in Genome Res. 10 (5), 703-713 (2000) 1140 1200 1200 1260 1260 GAGGGAGGGGCTTGTTTCCCTTCCCTCCGGCGACAAGCTCCAGGGCAGGCTGTGCCT 1320 1320 1380 1440 CTGTGTTTGGTGGGGGGATGTCTCCAGGAACCAAGAGCCCTCAGCCTGGTGTAGT 1500 ATGGAGGCTGTGAGTGAACCCCCTGCATGTGGACTCCACCTGGCTGCTGCTGCTGCGGAGG GCTGCCCCCCCCTGTGCATCAGACCTATGAGTTCGGCAAAAGCTTCTTCGAG AGGCTGAACCAGGACCGGCTTCTGGGCGGCTGAAAGGGGCCAAGGAGGCAAGGACCCCGTC CTGGGGGGCCCAGCACTICCTCAGACACACTICCTGCTGCTCCAGTCGTGGGGGATC TCTCCCACGGATGGGGAGAGGGGGAGGAGCCCAGCCAAGTGCCTTTTCCTCA3CACT AICACTIACCCACCCCCCAAGITCAAGACCAAAICTICCAGCTGCCCCTTCGTGTTTCC NAIDLES?/
Homo sapiens CGI-69 protein mRNA, complete cds.
AF151827 CICCUTGACCCTTGATTCCTTAAGTCTAAGATGATGAACTTC 1546 1. .1556 /organism="Homo sapiens" /db\_xref="taxon:9606" /chromosome="17" 118. .1173 AF151827.1 GI:4929606 (bases 1 to 1556) Homo sapiens. Homo sapiens 10810093

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BC001398 15-70 bp mRNA linear PRI 12-JUL-2001 Homo sapiens, CGI-69 protein, clone MGC:1163 IMAGE:3051436, mRNA, complete cds.
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Submitted (12-DEC-2000) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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VPFSALLYFPWYELVKSWLNGFRPKDGTSVGMSFVAGGISGTVAAVLTLPFDVVKTQRQ
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This clone was selected for full length sequencing because it passed the following selection criteria: marched mRNA gl: 10438782.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translation="MADQDPAGISPLQQMVASGTGAVVTSLFMTPLDVVKVRLQSQRP"
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dlone="WGC:1163 IMAGB:3051436"
tissue type="Colon, adenocarcinoma"
clone lib="WIH MGC 15"
lab_host="DH108-R"
Library Preparation: Rubin Laboratory
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Location/Qualifiers
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/product="Unknown (protein for MGC:16684)"
/protein id="MAH09330.1"
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/translation="WABODPAGISPLOQMVASGTGANVTSLEMTPLDVVKVRLQSQRPSMASEMPESRLWSLSYTRWKCLLYCDVGVLEPLYLCPNGARCATWFQDPTRFTGMDAFVKIVRHBGTRTLWSGLBATLWWFVRAPATALFTRAYDQLARFCCRALTSDLYAPWVAGAALARLGTVTVTSLSPLEMMFTKLQAQHVSYREIGACVRTAVAQGGMRSLALGGGPTRALBG
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VALGANBTRAYNPLHVDSTWLLLRRIRAESGTKGLFAGFLRFITKAAPSCAIMISTYB
                                                                                                                                                                                                                                                 Craniata; Vertebrata; Buteleostomi;
Catarrhini; Hominidae; Homo.
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1450 TICCCIGIGITIGCTGIAGCIGGCAIGITCTCCAGGAACCAAGAAGCCCTCAGCCTGGTG 1509
                                                                                                                                             BCUU9330
Homo sapiens, clone MGC:16684 IMAGE:4126268, mRNA, complete cds.
BC009330
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Contact: MGC help desk
Email: egapbs-rémail.nih.gov
Tissue Procurement: ATC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                            1497 TAGTCTCCCTGACCCTTGTTAATTCCTTAAGTCTAAAGATGATGAACTTC 1546
                                                             1510 TAGTCTCCCTCACCCTTGTTAATTCCTTAAAGTCTAAAGATGAAGTTC 1559
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-(done="MGC:16684 IMAGE:4126268"
-(tissue_type="Brain, neuroblastoma"
-(clone_tib="NHH MGC 19"
-(lab_host="DH10B-R"
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Submitted (12-JUN-2001) National Institutes
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Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

(bases 1 to 1550)

Wiemann, S., Well, B., Wellenreuther, R., Gassenhuber, J., Glassl, S., Ansorge, W., Boecher, M., Bloecker, H., Bauersachs, S., Bluu, H., Lauber, J., Duesterhoeft, A., Beyer, A., Koehrer, K., Strack, N., Mewes, H. W., Ottenwaelder, B., Obermaler, B., Tampe, J., Heubner, D., Wambutt, R., Korn, B., Klein, M. and Poustka, A.

Toward a Catalog of Human Genes and Proteins: Sequencing and Analysis of SON Novel Complete Protein Coding Human cDNAs
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Homo sapiens mRNA; cDNA DKFZp434C119 (from clone DKFZp434C119);
complete cds.
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POUSTKA,A., Klein,M., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
Direct Submission
Submitted (15-DEC-1999) MIPS, Am Klopferspitz 18a, D-82152
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Clone from S. Wiemann, Molecular Genome Analysis, German Car
Research Center (DKF2); Email s.wiemann@dkfz-heidelberg.de;
sequenced by DKFZ (German Cancer Research Center,
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/tränslation="MADQDPAGISPLOQMVASGTGAVVTSLFMTPLDVVKVRLQSG..
SMASELMPSSRLWSLSYTKWKCLLYCNGVLPPLYLCPNGARCATWFQDPTRFTGTMDA
FVKIVRHEGTRTLWSGLPATLVMTVPATAIYFTAYDQLKAFLCGRALTSDLYAPMVAG
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VPFSALYMFNYELVKSWINGLRPKDOTSVGMSFVAGGISGTVAAVITLPFDVVKTORO
VALGAMEAVRVNPLHVDSTWLLLRRIRAESGTKGLFAGFLPRIIKAAPSCAIMISTYE
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                                                                                                                                                                                                 /gene="DKFZp434Cl19"
/note="CGI-69 protein, strong similarity to mitochondrial
carrier proteins"
                                                               /clone="DKFZp434cl19"
//Lissue type="testis"
/clone_lib="434 (synonym: htes3). Vector pSport1; host
DH10B; sites NotI + SalI"
/dev_stage="adult"
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/protein_id="CA863728.1"
/db_xref="G1:6599170"
/db_xref="SPTREMBL:Q9UF66"
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              /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                            Homo sapiens cDNA: FLJ22407 fis, clone HRC08407.
AK026060.1 GI:10438782
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DEFINITION ACCESSION VERSION

RESULT 6 AK026060 LOCUS

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2 (bases 1 to 1554)
Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Isogai, T.,
Shibahara, T., Tanaka, T. and Nakamura, Y.
Direct Submission
Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboracory of Genome Structure Analysis, Human
Genome Center: Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8619,
Fax:81-3-5449-5416)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MADODPAGISPLOQMVASGTGAVVTSLFMTPLDVVKVRLGSGRP
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Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T.,
Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
NEDO human cDNA sequencing project
                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'-& 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly S' ported by Science and Technology
                      Homo sapiens primary human renal epithelial cells cDNA to mRNA, clone_lib:HRC clone:HRC08407.
Homo sapiens
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/clone_lib="HRC"
/note="cloning vector pME18SFL3"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HRC08407"
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/db_xref="G1:10438783"
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1394 CCCCCAAGTICAAGACCAAATCTTCCAGCTGCCCCTTCGTGTTTCCCTGTTTTGCTGT 1453
                                               1454 AGCTGGGCATGTCTCCAGGAACCAAGAAGCCCTCAGCCTGGTGTAGTCTCCCTGACCCTT 1513
                                                                                                                                                                                                                                                             Unknown.
Unclassified.

1 (bases 1 to 1643)
Lal,P., Hillman,J.L., Bandman,O., Shah,P., Au-Young,J., Yue,H.,
Guegler,K.J. and Corley,N.C.
Human regulatory molecules
Patent: US 6132973-A 68 17-OCT-2000,
Location/Qualifiers
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               1394 CCCCCAAGTICAAGACAAAICITCCAGCTGCCCCTTCGTGTTTCCCTGTGTTTGCTGT
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                                                                                                                Query Match
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(Rel. 63, Created) (Rel. 67, Last updated, Version 2)

12-MAY-2000 09-MAY-2001 AF119864.1

Homo sapiens PRO2163 mRNA, complete cds

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                                                      727 GAGCTTATGCGGACAAAGCTCCAGGCTCAGCATGTGTCGTACCGGGAGCTGGGTGCCTGT
                                                                                                                                                                GTTCGAACTGCAGTGGCTCGGGTGGCTGGCGCTCACTGTGGCTGGGCTGGGCCCCACT
                                                                                                                                                                                                              847 GCCCTTCGAGATGTGCCCTTCTAGCCCTGTACTGGTTCAACTATGAGCTGGTGAAGAGC
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standard; RNA; HUM; 1402

AF119864; AF119864

RESULT 8
AF119864
ID AF11
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AC AF11
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                                                                                                                                                                                                 Zhang C., Yu Y., Zhang S., Wei H., Zhang Y., Zhou G., Bi J., Liu M., He F.; "Functional prediction of the coding sequences of 79 new genes deduced by unpublished.
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Department of Experimental Hematology, Institute of Radiation Medicine,
Beljing Taiping Road 27, Beljing, Beljing 100850, P. R. China
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157 CAAATGGTGGCCTCAGGCACCGGGGCTGTGGTTACCTCTCTTCATGACACCCCTGGAC 216
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                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="liver"
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4. .1017
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                                                                                                                                                                                                                                                                                                                                                                                                SWISS-PROT; Q9BZJ4; CG69_HUMAN
                                                                                                                            Homo sapiens (human)
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Local Similarity
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77 GGSCAAGGAGGAAGGACCCGTCTCTCCCAGGATGGGAAGAGGGAAGAGAGAAACCA 123 	Qy Db
17 GAG     61 GAG	Oy Dp
57 GGCTTCCTCGTGGATCATCAAGGCTGCCCCTCCTGTGCCATCATGATCAGCCCTAT 11	g S
TIGGCTGCTGCTGCGGAGGATCGGGGCCGAGTCGGGCACCAAGGGACTCTTTGCA 1	Oy Dp
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7 GGTGGCATCTCAGGGACGGTGGCTGCAGTGCTGACTCTCTCT	oy Dio
7 AGCTGGCTCAATG	Qy Dp
CCTTCGAGATGTGCCCTTCTCAGCCCTGTACTGGTTCAACTATGAGCTGGTGAAG 8	Qy Dp
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457 ACCTCTGGAGCGGCCTCCCCGCCACCCTGGTGATGACTGTGCCAGCTACCGCCATCTAC 516	S G
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
105 CTGAAGCTTCAAGATGGCTGACCAGGACCCTGGGGGCATCAGCCCCTCCAGGAAATGGT 164
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Cgi-69 compositions and methods of use
Patent: Wo 0198355-A 1 27-DEC-2001;
Genentech, Inc. (US); Curagen Corporation (US)
Location/Qualifiers
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1 349 c 332 g 239
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Sequence 1 from Patent W00198355,
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AX403084.1 GI:21388033
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Yu,X.X., Lewin,D.A., Zhong,A., Brush,J., Schow,P.W., Sherwood,S.W., Pan,G. and Adams,S.H.
Overexpression of the human 2-oxoglutarate carrier lowers mitochondrial membrane potential in HEX-293 cells: contrast with the unique cold-induced mitochondrial carrier CGI-69
Biochem. J. 353 (Pt 2), 369-375 (2001)
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Yu,X.X., Lewin,D.A., Zhong,A., Brush,J., Schow,P.W., Sherwood,S.W.
Pan,G. and Adams,S.H.
Direct Submission
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Homo sapiens mitochondrial carrier protein CGI-69 long form mRNA,
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/db xref="GI-12620400"
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RFTGTMDAFVKIVRHEGTRTLMSGLAPATLOWTVPATAIVFTATPDQLKARELGGRALTSD
LYAPWYAGALARICOTTVVISPLELMATRACHQAQHYSYRELGACVRTAVAQGGWRSLWLG
WGPTALRDVPFSALYWFNYELVKSWLNGLRPKDQTSGVGWRSLWLG
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Pred. No. 2.6e-222;
0; Mismatches 1;
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97.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC098934 173434 bp DNA linear HTG 06-NOV-2001
Homo satiens chromosome 1 clone RP11-480112, WORKING DRAFT
SEQUENCE, 6 unordered pieces.
AC098934 AL390963
AC098934.1 GI:16751904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryoca, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                 CCCCCTGCATGTGGACTCCACCTGCTGCTGCGGAGGATCCGGGCCGAGTCGGGCAC 1040
                                                                                                                                                                                                                                        1100
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                                                                                                                                                                                                                                                                                                                                               1021 CATGATCAGCACCTATGAGTTCGGCAAAAGCTTCTTCCAGAGGGTGAACCAGGACCGGCT 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (06-NOV-2001) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA.
On Nov 6, 2001 this sequence version replaced g1:13157584.
                                                                                  841 TGACGTGGTAAAGACCCAACGCCAGGTCGCTCGGGAGCGATGGAGGCTCTGTGAGAGTGAA 900
                                                                                                                                                                           901 CCCCCTGCATGTGGACTCCACCTGGCTGCTGCGGAGGATCCGGGCCGAGTCGGGCAC
781 CATGAGCTTTGTGGCTGGTGGCATCTCAGGGACGGTGGCTGCAGTGCTGACTCTACCCTT 840
                                              TGACGTGGTAAAGACCCAACGCCAGGTCGCTCTGGGAGCGATGGAGGCTGTGAGAAGTGAA 980
                                                                                                                                                                                                                            CAAGGGACTCTTTGCAGGCTTCCTTCGTCGATCATCAAGGCTGCCCCCTCTGTGCCAT
                                                                                                                                                                                                                                                                                                                   CATGATCAGCACCTATGAGTTCGGCAAAAGCTTCTTCCAGAGGCTGAACCAGGACCGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTG, HTGS_PHASE1; HTGS_DRAFT, HTGS_FULLTOP, HTGS_ACTIVEFIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality coverage: 8.7x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing vector: plasmid; 32% of reads
Sequencing vector: plasmid; L08752; 68% of reads
Chemistry: Dye-terminator ET; 89% of reads
Chemistry: Dye-terminator ET; 89% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 17058 bases at least Q40
Consensus quality: 17529 bases at least Q30
Consensus quality: 175299 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: University of Washington Genome Center
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Kaul, R. K., Olson, M. V., Raymond, C. and Haugen, E. D.

Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 173434)
Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.
Direct Submission
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Contact: uwgchtgs@u.washington.edu
Drafting Center: SC
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Center clone name: RP11-480112 (sc0719)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129 GGACCCTGCGGGCATCAGCCCCCTCCAGCAAATGGTGGCGCTCA-GGCACCGGGGCTGTGG 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       247 CCCTCCATGGCCAGCGAGCTGATGCCTTCCTCCAGACTGTGGAGCCTCTCTATACGAAA 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        307 IGGAAGIGC-----CICCIGIATIGCAAIGGIGICCIGGAGCCICTGIACCIGIGCC 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 GCGCCGCCGCACGAGCACCAGCCTAGAGCCAGGACTGAAGCTTCAAGATGGCTGACCA 128
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Pred. No. 2e-163;
0; Mismatches 282; Indels 60; C
                   1 9114: contig of 9114 bp in length 9115 27205: contig of 17991 bp in length 7206 27305: gap of unknown length 1306 47651: contig of 17991 bp in length 7652 47751: gap of unknown length 74121: contig of 20346 bp in length 74121: contig of 26370 bp in length 7422 112038: contig of 37817 bp in length 12186: gap of unknown length 121938: gap of unknown length 121938: contig of 37817 bp in length 1219434: contig of 18206 bp in length 122026: gap of unknown length 122039 112138: gap of unknown length 122039 112138: gap of unknown length 1239 112138: gap of unknown length 12204344: contig of 61296 bp in length.
                                                                                                                                                                                                                                                                              1. .173434
/organism="Homo sapiens"
/dz_xef="taxon:9606"
/dbromosome="1"
/clone="RP11-480112"
/clone="RP11-480112"
/clone="RPCI human BAC library ll"
|1. .9114
/note="assembly_name:Contig112"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27306. .47651
/note="assembly_name:Contigl14"
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/note="assembly_name:Contig115"
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/note="assembly_name:Contig113"
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Best Local Similarity 77.5
Matches 1176; Conservative
* be preserved.
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599 COCTGGCCCGCCTGGGCACCGTGACTG---TGATCAGCCCCCTGGAGGTTATGCGGAGAA 655
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                              16088 IGCIGGICCACCCIGGCACTAICACIGCAAICAICAGIGCCCIGGAGGITAIGCAGACAA
                                                              656 AGCTGCAGGCTCAGCATGTGTCGTACCGGGAGCTGGGTGCCTGTGTTCGAACTGCAGTGG
                                                                                                                              CTCAGGGTGGCTGGCGCTCACTGGGCTGGGCCCCCACTGCCCTTCGAGATGTGC
                                                                                                                                                                                                                                                         836 GECCGAAGGA------CCAGACTICTGTGGGCATGAGCTTTGTGGCTGGTGGCA
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HTG 24-JUL-2002

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Rature
Rattus norvegicus clone CH230-75J9, *** SEQUENCING IN PROGRESS ***,
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (24-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA on Jun 17, 2002 this sequence version replaced gi:21397217.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'eb site: http://www.hgsc.bcm.tmc.edu/
'ontact. hgsc-help@bcm.tmc.edu
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HTG; HTGS_PHASE1.
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                                                                                                                                                                                                                            NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.html). NOTE: This is a 'working draft' sequence. It currently consists of 60 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                      Sequencing vector: Plasmid; Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329 consensus quality: 143647 bases at least Q40 Consensus quality: 149058 bases at least Q30 Consensus quality: 153360 bases at least Q20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus clone CH230-161G12, *** SEQUENCING IN PROGRESS ***, 66 unordered pieces.
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73366 GCACCAAGA-GCTGACTCCACCTGCTTCAGAGAATCCAGGCTGAATCTGGCAC 73424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  981 CCCCCTG ATGTGGACTCCACCTGGTGCTGCTGCGGAGGATCCGGGCCGAGTCGGGCAC 1040
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1101 CATGATCAGCACCTATGAGTTCGGCAAAAGCTTCTTCCAGAGGGTGAACCAGGACCGGCT 1160
622 ACTGIGATCAGCCCCCTGGAGCTIAIGCGGACAAAGCTGCAGGCTGAGGATGTGTGGTAG 681
                                                                                            742 CTGGGCTGGGGCCCCACTGCCCTTCGAGATGTGCCCTTCTCAGCCCTGTACTGGTTCAAC 801
                                                                                                                                                                                                                                                                                                            861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 921 TGACGIGGIAAAGACCCAACGCCAGGTCGCTCTGGGAGCGATGGAGGCTGTGAGAGTGAA 980
                                                                                                                                                                                                                                                                                        802 TATGAGGTGGTGAAGAGCTGGCTCAATGGGTTCAGGCCGAAGGACCAGACTTCTGTGGGC
                                                                                                                                                                                                                                                                                                                                                                                  862 AIGAGCITIGIGGCIGGIGG-CAICTCAGGGACGGTGGCIGCAGIGCIGACICTACCCIT
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Rattus norvegicus
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Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L. E., Katobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Katly, S., Khan, U., King, L., Kovah, J., Kovar, C., Katovic, J., Kuchiy, S., Khan, U., King, L., Kovah, J., Kovar, C., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, M., Loulseged, H., Lozado, R. J., Lu, X., Lucier, R., Luna, R., Marinez, E., Mawhiney, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M. P., Meador, M., Mei, G., Morris, S., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Mayen, N., Nowetson, S., Oquh, M., Okwnon, G., Petirs, D., Pickens, R., Primus, E., Pu, L. L., Quiles, M., Ren, Y., Primus, E., Pu, L. L., Quiles, M., Ren, Y., Scherer, S., Scott, G., Shan, H., Shooshtari, N., Stsson, I., Soderer, S., Soatek, R., Tabor, P., Tamerisa, R., Tamerisa, R., Tang, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, R., Tames, S., Warlington, S., Walliams, G., Walliams, G., Walliams, G., Walliamson, A., Walczyk, R., Wooden, S., Worley, K., Wu, Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (19-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (13-JUL_2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA on Jul 12, 2002 this sequence version replaced gi:18701120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Assembly program: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 99973 bases at least 040 Consensus quality: 106615 bases at least 030 Consensus quality: 111100 bases at least 020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1025: contig of 1025 bp in length
1125: gap of unknown length
1218: gap of unknown length
2318: gap of unknown length
3454: contig of 1136 bp in length
4600: contig of 1136 bp in length
4790: gap of unknown length
4790: gap of unknown length
5955: contig of 1155 bp in length
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Contact: hgsc-help@bcm.tmc.edu
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Center clone name: CH230-161G12
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77121 ACTGCTATGGTGTCCTGGACCTGTGCCCGAATGATAGTACTCGCTGCGCCACCT 77180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77181 GGTTTCAGGATCCTACAAGGTTTACTGGCACCTTGGATGCCTTTGTGAAGATTGTGAGGC 77240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 537.2; DB 2; Length 156175;
Pred. No. 2.5e-108;
0; Mismatches 183; Indels 22; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  323 ATTGCAATGGTGTCCTGGAGCCTCTGTACCTGTGCCCAAATGGTGCCGCTGTGCCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    443 ACGAGGACCAGGACCTTCTGGAGGGGCCTCCCGGCCACCTTGGTGATGACTGTGCCAG
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Best Local Similarity 77.6%;
Matches 709; Conservative
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Worley, K.C.

Worley, K.C.

Bixect Submission

Submitted (29-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 29 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (13-4UL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 3, 2002 this sequence version replaced gi:21239891.
  Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstock,G. and Gibbs,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chamistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329 consensus quality: 108533 bases at least Q40 consensus quality: 111720 bases at least Q30 consensus quality: 1113548 bases at least Q20
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1534: gap of unknown length
3218: contig of 1684 bp in length
3318: gap of unknown length
4531: contig of 1213 bp in length
6531: gap of unknown length
5802: contig of 1171 bp in length
5902: gap of unknown length
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23210: contig c
23310: gap of u
25515: contig c
25615: gap of u
27411: contig o
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Albases I to 128802)

Albascoks.L. Addo-Oduola, B., Ali-Osman, F.R., Allen, C., Albaria, J., Benden, C., Addo-Oduola, B., Ali-Osman, F.R., Allen, C., Barbaria, J., Benden, J., Binage, K., Blankenburg, K., Bonnin, D., Babdaria, J., Benden, J., Binage, K., Blankenburg, K., Bonnin, D., Babday, C., Burch, E., Burker, M., Erown, M., Bryank, N.C., Carren, M., Cavazos, S.R., Chacko, J., Chavez, D., Caren, M., Cavazos, S.R., Chacko, J., Chavez, D., Caren, M., Chen, Z., Chowdhry, I., Chacko, J., Chavez, D., Cave, Carrell, M. L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H. H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H. H., Delaney, K.R., Delgado, D., Flagga, N., Foster, P., Frantz, P., Falls, T., Ferraguto, D., Flagga, N., Foster, P., Prantz, P., Garris, J., Gavara, M., Guner, T., Garza, N., Gill, R., Garris, M., Gao, J., Garcia, A., Ganer, T., Garza, N., Gill, R., Harris, C., Howest, M., Harris, C., Herris, K., Harris, K., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Lucier, R., Luna, R., Martinez, E., Mahris, M., Martinez, E., Kalty, J., Martinez, R., Lucier, R., Luna, R., Mayon, N., Martinez, R., Markinez, E., Mahris, M., Martiney, E., Markiney, ., Martiney, E., Markiney, E., Soctt, G., Sherry, March, Soctt, G., Sherry, R., Stone, H., Shockhar, R., Pase, M., Taylor, T., Taylor, T., Taylor, T., Taylor, T., Taylor, T., Taylor, T., Taylor, T., Taylor, T., Taylor, T., Taylor, T., Taylor, Mang, S., Wang, S., Wang, S., Wang, S., Wang,
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128802 bp DNA linear HTG 13-JUL-2002
Rattus norvegicus clone CH230-11K3, *** SEQUENCING IN PROGRESS ***,
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1: gap of unknown length
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7: contig of 2758 bp in length
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Bukaryota, Metaroa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 537)
Xu.J., Skeiky, Y.A., Reed, S.G. and Cheever, M.A.
Compositions and methods for therapy and diagnosis of prostate cancer
                                                                             77585 CTTAACCTCTGACCTCTACGCACCCATAGTAGTGCTGCTTCGGCTGAATGGGCATTGT 77526
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Human CGI-69 cDNA Human cDNA for nov Monse ischaemic co	#1133 used t	ORFX ORF22	1179 used		CDNA encodi	cDNA encoding nove	ο.	Human gene signatu	Human polynucleoti	Human colon cancer	Drosophila melanod	Drosophila melanog	Murine transport a	Drosophila melanog	Drosophila melanog	Drosophila melanog	Human polynucleoti	Human foetal liver	Human brain expres	Human bone marrow	Probe #7739 used t	genome-d	Human foetal liver	ă	m euc	_	qenome-deri	e apoptosis	encoding mur	cell cDNA	ne cDNA isola
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## ALIGNMENTS

CG1-69, mitochondrial carrier protein, human, metabolic disease, obseity; cachexia, tumour, cancer; infection; immunomodulator; antitumour; virucide; antibacterial; anorectic; antidiabetic; brown adipose tissue; diagnosis; gene therapy; ss. Human mitochondrial carrier protein CGI-69 cDNA. Location/Qualifiers 118..1173 /\*tag= a AAI71020 standard; cDNA; 1546 BP. 18-MAR-2002 (first entry) Homo sapiens. 

WO200198355-A2

27-DEC-2001.

22-JUN-2001; 2001WO-US20117.

22-JUN-2000; 2000US-213307P.

(GETH ) GENENTECH INC. (CURA-) CURAGEN CORP.

N

Yu XX; Adams SH, Lewin D,

WPI; 2002-114569/15

CGI-69 polypeptides and polynucleotides useful for treating metabolic disorders including cachexia, obesity, diabetes and cancers -

Disclosure; Page 11-12; 107pp; English.

splice variant) nuclein acids and proteins are useful for diagnosing and treating metabolic diseases in humans, including obesity, cacheria and diabetes. Evidence for an important function for CGI-69 in modifying mitochondrial membrane potential in brown adipose tissue (BAT) is presented. The mouse orthologue of CGI-69 is up-regulated in cold-treated BAT. CGI-69 may be involved in cellular thermogenic uncoupling and, therefore, may be used to diagnose and treat specific perturbations in metabolic pathways. Altering the expression of CGI-69 through gene therapy provides a means of treating metabolic diseases, such as obesity or cachexia, or of increasing or decreasing body weight. Decreasing the or of increasing or decreasing body weight. Decreasing the activity of CGI-69 can be used to treat cachexia, tumours, cancers, viral infections and bacterial infections, while increasing its activity can be used to treat obesity, tumours, cancers, viral infections and bacterial infections (all claimed). Methods are The present sequence is that of cDNA encoding human CGI-69 (see AAMSOSTO). Various CGI-69 clones were isolated from human liver upon PCR amplification and cloning. Some diverged from the previously known CGI-69 sequence in that they encoded an 8-amino acid insert preceded by a W64L change, and were termed the 'long version' isoform or CGI-69. (see AAT71019). The invention relates to a novel characterization of CGI-69 as a mitochondrial carrier protein, the discovery of CGI-69. (and the discovery of the alteration of the mitochondrial membrane potential through overexpression of carboxyl FLAG-tagged CGI-69. CGI-69 (including also claimed for determining whether a compound up-regulates or down-regulates expression of a CGI-69 gene, and of screening for mutation in the CGI-69 gene. 

Sequence 1546 BP; 272 A; 489 C; 459 G; 326 T; 0 other;

.; 0 180 240 240 300 360 420 420 61 GGCCCTGGGCGCCGCGCCGCACGAGCACCAGCCTAGAGCCTGAAGCTTCAAGATG 120 GGCCCTGGGCGCCGCGCGCGCGCGCCCTAGAGCCAGGACTGAAGCTTCAAGATG 120 121 gergaccaggacergeggecarcagecerecegeaangergecereaggacegeg 180 241 CAGCGGCCCTCCATGGCCAGCGAGCTGATGCCTTCCTCCAGACTGTGGAGCCTCTCCTAT 300 ACCAAATGGAAGTGCCTCCTGTATTGCAATGGTGTCCTGGAGCCTCTGTACCTGTGCCCA 360 421 GCCTTCGTGAAGATCGTGAGGCACGAGGCACCAGGACCCTCTGGAGCGGCCTCCCCGCC 480 Gaps GGCTAGGTGCGCTGCGAGCGCGCGGAGCCACGAGGCGGACGACGTAATGGGCCCGCCT 60 9 361 AATGGTGCCCGCTGTGCCACCTGGTTTCAAGACCCTACCCGCTTCACTGGCACCATGGAT 1 GCCTAGGTGCGCTGCGAGCGCGCGCGCGAGGGCGGACGACGACGTAATGGGCCCCCT GCTGTGGGTTACCTCTCTCTCTATGACACCCCTGGACGTGAAGGTTCGCCTGCAGTCT CAGCGGCCCTCCATGGCCAGCGAGCTGATGCCTTCCTCCAGACTGTGGAGCCTCTCCTAT ACCAAATGGAAGTGCCTCCTGTATTGCAATGGTGTCCTGGAGCCTCTGTACCTGTGCCCA AATGGTGCCCGCTGTGCCACCTGGTTTCAAGACCCTACCCGCTTCACTGGCACCATGGAT GCTGACCAGGACCCTGCGGGCATCAGCCCCCTCCAGCAAATGGTGGCCTCAGGCACCGGG GCTGTGGGTTACCTCTCTCTTCATGACACCCTGGACGTGGAGGTTCGCCTGCAGTCT 100.0%; Score 1546; DB 24; Length 1546; 100.0%; Pred. No. 0; .; 0 0; Indels 0; Mismatches Matches 1546; Conservative Best Local Similarity Query Match 361 61 181 241 301 301 121 181 ò qq g ò qq ò qq ò qq ð D. ò q ò

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& 8	481	ACCCIGGIGAIGACIGIGCCAGCIACCGCCAICTACTICACIGCCIATGACCAACTGAAG 540
<i>ک</i> و ج	541	CGCACCCATGGTGGCTGGCGG 60
3 3	109	GGCCCCCCTGGGCCCCGGGCTGGCCCCCTGGGCCTTATGCGGCCGCCCCTGGCCGCCCCTGGCCGGCC
QC ,	109	TGGCCCGCCTGGGCACCGTGACTGATCAGCCCCTGGAGCTTATGCGGACAAAGCTG 66
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ò	38	TACCCACCCCCAAGTTCAAGACCAAATCTTCCAGCTGCCCCTTCGTGTTTCC 144
Q Q	1381	CACTTACCCACCCCCAAGTTCAAGACCAAATCTTCCAGCTGCCCCCTTCGTGTTTC
රු සි	1441	CTGTGTTTGCTGTAGCTGGGCATGTCTCCAGGAACCAAGAAGCCCTCAGCCTGGTGTAGT 1500
λō	1501	CICCUGACCCTIGITAATICCTIAAGACTAAAGATGAACTIC 1546

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                                                                                                                                                                                        Human, uncoupling protein; immunosuppressive; antiarthritic;
antirheumatic; antiproliferative; cardiant; vasotropic;
cerebroprotective; neuroprotective, antibacterial; opthalmological;
gastrointestinal; nephrotropic, gynaecological; vulnerary; thrombolytic;
gene therapy; cancer; wound; infectious disease; thrombosis; arthritis;
infertility; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is one of eighteen isolated nucleotide sequences encoding uncoupling proteins. The nucleotide sequences may be used for identification of various disorders such as cancer, for chromosome dentification, as chromosome markers and for numerous other diagnostic or research purposes. The uncoupling protein encoded by the nucleotide muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders, wounds, infectious diseases, thrombosis, arthritis, and infertility.
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CTCCCTGACCCTTGTTAATTCCTTAAGTCTAAAGATGATGAACTTC 1546
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                                                                                                                                                          Human uncoupling protein cDNA
                                                                       AAC90452 standard; cDNA; 1560
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99US-0142821.
99US-0149448.
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Best Local Similarity 98.8%;
Matches 1510; Conservative
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antianaemic; gene therapy; cancer: proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; burn, manaemia; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipscriatic; antiparkinsonian; noctropic; neuroprotective; anticonvulsant; oscepathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coaqulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; antiviral; antibaccerial; antifungal; intiheumatic; antithrough;
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                       1276 TGTTTCCCTTCCCGGGGGGAGGTCCAGGGAGGGCTGTCCCTGGGGGGCCAG
                                                               1334 CACTICCICAGACACAACTICTICCIGCIGCICCAGICGIGGGGATCAICACTTACCCAC
                                                                                          1336 CACTICCTCAGACCACAACTICTTCTTCTTCTTCCAGTCGTGGGGATCATCACTTACCCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human ORFX ORF2547 polynucleotide sequence SEQ ID NO:5093.
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99US-0127636.
99US-0127728.
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which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cycostatic; hepatotropic; vulnerary; cardiatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunosuppressant; immunosuppressant; immunosuppressant; immunosuppressant; immunosuppressant; immunosuppressant; immunosuppressant; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antiniflammatory; antibacterial; antivinal; antichnugal; anticheumatic; antithrianamic. The sequences can be used for determining pathological conditions associated with an ORPX-associated disorder. The proposition to, or preventing or treating nucleic acids can be used to express ORFX proteins in gene therapy.

Control of a conditions associated with an ORPX-associated disorder. The proteins and nucleic acids may be used to treat cancers, or proliferative disorders, neurodegenerative disorders, neurodegenerative disorders, neurodegenerative disorders, neurodegenerative disorders, systemic tythematosus, severe combined immunodeficiency (SCID), AIDS, viral, expertension, hypothyroidism, cholesterol ester storage, systemic lupus cortinal hemoglobinuria, burns, wounds, bone and cartilage damage, concturnal hemoglobinuria, antiinflammatory disease; to enhance concurse the contraceptive.
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TGACTGTGATCAGCCCCTGGAGCTTATGCGGACAAAGCTGCAGGCTCAGCATGTGTCGT 679

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CGI-69L; mitochondrial carrier protein; human; metabolic disease, obesity; cachexia; tumour; cancer; infection; immunomodulator; antitumour; virucide; antibacterial; anorectic; antidiabetic; brown adipose tissue; diagnosis; gene therapy; splice variant; ss.

Location/Qualifiers 14..1093

Homo sapiens

Key CDS

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WO200198355-A2.

27-DEC-2001.

22-JUN-2001; 2001WO-US20117 22-JUN-2000; 2000US-213307P

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                  AGGACCAGACTTCTGTGGGCATGAGCTTTGTGGCTGGCGATCTCAGGGACGGTGGCTG
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metabolic

CGI-69 polypeptides and polynucleotides useful for treating disorders including cachexia, obesity, diabetes and cancers

Yu XX;

Lewin D, Adams SH, WPI; 2002-114569/15. P-PSDB; AAM50569

GENENTECH INC. CURAGEN CORP.

(GETH ) (CURA-)

Claim 1(a); Page 9-10; 107pp; English.

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The present sequence is that of cDNA encoding human CGI-69L (see AMNSO569), a novel splice variant of human CGI-69. Various CGI-69 clones were isolated from human liver upon PCR amplification and clones where isolated from the previously known CGI-69 cloning. Numerous clones diverged from the previously known CGI-69 cloning. Numerous clones diverged from the previously known CGI-69 w44L change, and were termed the 'long version' isoform or CGI-69. The invention relates to a novel characterization of CGI-69, and the cut cochondrial carrier protein, the discovery of CGI-69L, and the discovery of the alteration of the mitochondrial membrane potential chrough overspression of carboxyl-FLAG-tagged CGI-69. CGI-69. Coloning splice variant) nucleic acids and proteins are useful concluding splice variant) nucleic acids and proteins are useful concluding splice variant) nucleic acids and proteins are useful concluding splice variant) nucleic acids and proteins are useful conceptly, cachexia and diabetes. Evidence for an important function of the colludar thermogenic uncoupling mitochondrial membrane potential in brown adipose tissue (BAT) is presented. The mouse orthologue of CGI-69 colludar thermogenic uncoupling and, therefore, may be used to diagnose and treat specific perturbations in metabolic pathways. CG activity of CGI-69 can be used to treat cachexia, tumours, cancers, a criming the expression of CGI-69 through gene therzapy provides a crivity of CGI-69 can be used to treat cachexia, tumours, cancers, activity can be used to treat obesity, tumours, cancers, viral infections and bacterial infections, while increasing its activity can be used to treat obesity, tumours, cancers, viral also claimed for determining whether a compound up-regulates or a mutation in the CGI-69 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGAAGCTTCAAGATGGCTGACCAGGACCTGCGGGCATCAGCCCCCCTCCAAGAAATGGT 164
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Pred. No. 8.9e-250;
0; Mismatches 1;
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97.8%;
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Human mitochondrial carrier protein CGI-69L cDNA.

(first entry)

18-MAR-2002 AAI71019;

RESULT 4
AAI71019
ID AAI7
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AAI71019 standard; cDNA; 1114

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The present invention describes isolated polypeptides, comprising an immunogenic portion of a prostate tumour protain (PTP). The polypeptides and polymucleotides encoding them have cytestatic activity and can be polymucleotides encoding them, antigen presenting cells which express the polypeptides and in gene therapy. The polypeptides and in gene therapy. The polypeptides and can be used for inhibiting the development of prostate cancer in a patient. The polypeptides can be used for inhibiting the development of prostate cancer in a patient. The polypeptides can be used to generate antibodies or anti-didotypyic antibodies for passive immuno therapy. A portion of the polymucleotides encoding the polypeptides can be used as a probe or modulate the expression of the polypeptides. AAAN66241 to AAAN66691 and AAAN82020 to AAAN82020 represent sequences used in the exemplification of
                                                                                         tumour protein cDNA sequence SEQ ID NO:387,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1144
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                                                                                                               prostate cancer; diagnosis; tumour; gene therapy; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polypeptide useful for treating and diagnosing prostate cancer comprises an immunogenic portion of prostate tumor protein - \,
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Conservative 0, Mismatches
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                                                                                                                                immunogenic; cytostatic; vaccine; ss.
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       BP.
 AAA06606 standard; cDNA; 537
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98US-0116134.
98US-0159812.
98US-0159822.
99US-0232149.
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                                                                                   Human immunogenic prostate
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Best Local Similarity
Matches 522; Conserva
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                                                                                                                                                          Homo sapiens.
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14-JUL-1998;
23-SEP-1998;
23-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to isolated prostate-specific polypeptides, polypucides, tusion proceins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting cells argressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polyuclectides and the antigen-presenting cells are useful for stimulating and/or expanding
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                                         GCGGCCCAGCACTTCCTCAGACACATCTTCCTGCTGCTCCAGTCGTGGGGATCATCA 1384
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                            300
                                                            GCGGCCCAGCACTTCCTCAGACACAACTTCTTCCTGCTGCTCCAGTCGTGGGGATCATCA 360
                                                                                                                                    human prostate-specific polypeptides and polynucleotides useful diagnosis and treatment of cancer, especially prostate cancer -
   GAGGGGCTTGTTTCCCTTCCCTCCCGGCGACAAGCTCCAGGGCAGGGCTGTCCCTCTGG
                      CTTACCCACCCCCAAGTTCAAGACCAAATCTTCCAGCTGCCCCCTTCGTGTTTCCCTGT
                                                                                            CTTACCCACCCCCAAGTTCAAGACCAAATCTTCCAGCTGCCCCCTTCGTGTTTCCCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kalos MD;
Carter D;
                                                                                                                                                                                                                                                                                                            Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
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                                                                                                                                                              CTGACCCTTGTTAATTCCTTAAGTCTAAAGATGATGAACTTC 1546
                                                                                                                                                                            CTGACCCTTGTTAATTCCTTAAGTCTAAAGATGATGAACTTC 522
                                                                                                                                                                                                                                                                                          Human prostate cDNA sequence #357.
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2000US-0570737

2000US-0570737

2000US-063783.

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2000US-0651236.

2000US-0657279.

2000US-0657279.
                                                                                                                                                                                                                               AAS63815 standard; cDNA; 537
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12-MAY-2000; 2
13-UW-2000; 2
27-UW-2000; 2
59-AUG-2000; 2
66-SEP-2000; 2
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10-OCT-2000;
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    for a tumour protein, and for inhibiting the development
T cells specific for a tumour protein, and for inhibiting the developme of cancer especially prostate cancer. Compositions comprising the polypucleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The oligonucleotide is useful for detecting cancer. The present sequence is a prostate specific polymucleotide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 CCACGGATGGGGGAGAGGCAGGAGGACCCAGCCAAGTGCCTTTTCCTCAGCACTGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1385 CTTACCCACCCCCAAGTICAAGACCAAATCTTCCAGCTGCCCCCTTCGTGTTTCCCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTTTGCTGTAGCTGGGCATGTCTCCAGGAACCAAGAAGCCCTCAGCCTGGTGTAGTCTCC
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                                                                                                                                                                                                                Length 537;
                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                               Sequence 537 BP; 116 A; 167 C; 138 G; 116 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGACCCTTGTTAATTCCTTAAGTCTAAAGATGATGAACTTC 1546
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                                                                                                                                                                                                            ch 33.8%; Score 522; DB 22; I
il Similarity 100.0%; Pred. No. 8.7e-119;
522; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human prostate-specific cDNA sequence CGI-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytostatic; gene therapy; metastasis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAH93722 standard; cDNA; 537
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prostate-specific proteins (II). (I) and (II) have cytostatic activity,
and can be used in vaccine production and gene therapy. (I), (II),
and can be used in vaccine production and gene therapy. (I), (II),
antibodies to (II), fusion proteins comprising (II), and isolated
T cells prepared using (I) or (II) are used treat cancer in a patient.
C (I) and the antibodies are also used in the detection of cancer in a patient.
C (I) and the antibodies are is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used in vaccines. The antibodies or (I) can be used for monitoring the progression of cancer in a patient.
C (I) can be used for monitoring the progression of cancer in a patient.
C (I) and (II) can also be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. Adappage and Admostle to Admostle cancer to the present invention.
                                                                                                                                                                                                                                                                                                                      present invention describes polynucleotide sequences (I) which encode
                                                                                                                                                                                  New polynucleotide encoding a prostate-specific protein, for diagnosing, monitoring and treating prostate cancer in a patient and for use in vaccines -
                                                   St, Jiang Y, Reed SG;
Stolk JA, Skeiky YAW;
                                                 Harlocker SL
Retter MW,
                                                                                                                                                                                                                                                                     Claim 1; Page 359-360; 543pp; English.
                                          Dillon DC, Mitcham JL,
AD, Fanger GR, Day CH,
  (CORI-) CORIXA CORP.
                                                                                         Wang A, Meagher MJ;
                                                                                                                                   WPI; 2001-425873/45.
                                                                    Kalos MD,
                                               Xu J,
                                                                                                                                                                                                                                                                                                                      The
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Score 522; DB 22; Length 537; Sequence 537 BP; 116 A; 167 C; 138 G; 116 T; 0 other; Pred. No. 8.7e-119; Mismatches 0; 33.8%;

·; 1085 CCCCCTCCTGTGCCATCATCAGCACCTATGAGTTCGGCAAAAGCTTCTTCCAGAGGC 1144 1324 1205 CCACGGATGGGGAGGGCAGGAGAGCCCAGCCAAGTGCCTTTTCCTCAGGACTGAGG 1264 1384 1444 300 GTTTGCTGTAGCTGGGCATGTCTCCAGGAACCAAGAAGCCCTCAGCCTGGTGTAGTCTCC 1504 180 420 Gaps GTTTGCTGTAGCTGGGCATGTCTCCAGGAACCAAGAAGCCCTCAGCCTGGTGTAGTCTCC 480 TGAACCAGGACCGGCTTCTGGGCGGCTGAAGGGGGCAAGGAGGAGGCCCCGTCTCT CCACGGATGGGGAGGAGGAGGAGCCCAGCCAAGTGCCTTTTCCTCAGCACTGAGG 241 GAGGGGCTTGTTTCCCTTCCTTCCGGCGACAAGCTCCAGGGCAGGCTGTCCCTCTGG GCGGCCCAGCACTTCCTCAGACACAACTTCCTGCTGCTCCAGTCGTGGGGATCATCA 301 GGGGCCAGCACTTCCTCAGACACACATCTTCCTGCTGCTCCAGTCGTGGGGATCATCA CTTACCCACCCCCAAGTTCAAGACCAAATCTTCCAGCTGCCCCTTCGTGTTTCCCTGT 361 CTTACCCACCCCCAAGTTCAAGACCAAATCTTCCAGCTGCCCCCTTCGTGTTTCCCTGT GAGGGGCTTGTTTCCCTTCCCTCCGGCGACAAGCTCCAGGGCAGGGCTGTCCCTCTGG 0 0; Indels CTGACCCTTGTTAATTCCTTAAGTCTAAAGATGATGAACTTC 1546 CTGACCCTTGTTAATTCCTTAAGTCTAAGATGATGAGACTTC 522 33... 100.0%; Pre Matches 522; Conservative Query Match Best Local Similarity 1265 121 1325 1385 1445 1505 181 421 481 ò op ò a ò qq ð qq ò QQ ð QQ. ò qq ò a ò

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The present invention describes an isolated polypeptide (P1) comprising at least an immunogenic portion of a prostate specific protein, or its variant. Also described are polynuclectides (N1) encoding (P1). (P1) and The polypeptides, nucleic acids and antibodies from the present invention are useful in the diagnosis and therapy of prostate cancer. Invention are useful in the diagnosis and therapy of prostate cancer. In a genomic region on chromosome 1794P, P715P and B315D are located in a genomic region on chromosome 22411.2 known as the Cat Eye Syndrome relicon. Prostate specific antigen (PA) P501S was located on polynuclectide and polypeptide sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1085 CCCCCTCTGTGCCATCATGATCAGCACCTATGAGTTCGGCAAAAGCTTCTTCCAGAGGC 1144
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                                                                                                                                                                                                                                                                                                                                                                                                                                            an immunogenic portion of diagnosis and therapy of
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                                                                                                                            Human; prostate cancer; therapy; diagnosis; cat eye syndrome;
chromosome 22q11.2; prostate-specific protein; chromosome 1;
prostate specific antigen; PSA; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.8%; Score 522; DB 22; Length 537;
                                                                                                                                                                                                                                                                                                                                                                       Jiang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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Day CH, Skeiky YAW,
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                                                                                                   Human prostate-specific cDNA sequence CGI-69.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated polypeptide comprising at least prostate-specific protein, useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 31; Page 259; 325pp; English.
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dD, Retter MW, Stolk JA,
                AAH85036 standard; cDNA; 537 BP.
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nes 522; Conservative
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18-NOV-1999;
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                                           AAH85036;
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AAH02422 to AAH2872, AAB74798 to AAB74821 and AAB4830 are sequences cust in the exemplification of the present invention.
                                                                                                               1444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; prostate tumour antigen; prostate tumour; therapy; diagnosis; prostate cancer; immunogenic; cytostatic; vaccine; ss.
GAGGGGCTTGTTTCCTTCCCTCCCGGCGACAAGCTCCAGGGCAGGCTGTCTCTGG
                                                                   301 GCGGCCCAGCACTTCCTCAGACACATCTTCCTGCTGCTCCAGCGGGGGATCATCA
                                               GCGGCCCAGCACTTCCTCAGACACACTTCTTCCTGCTCCAGTCGTGGGGATCATCA
                                                                                                              CTTACCCACCCCCAAGTTCAAGACCAAATCTTCCAGCTGCCCCTTCGTGTTTCCCTGT
                                                                                                                                            361 crifacccaccccaagricaagaccaarcriccagcreccccritcergriccrer
                                                                                                                                                                             GITTGCTGTAGCTGGGCATGTCTCCAGGAACCAAGAAGCCCTCAGCCTGGTGTAGTCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 537 BP; 116 A; 167 C; 138 G; 116 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                        AAH02787 standard; cDNA; 537
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TGAACCAGGACCGGCTTCTGGGCGGCTGAAAGGGGCAAGGAGGCAAGGACCCCCTCTCTC 1204
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                                                                                                                                                                      reaaccaeeacceecrrcreeeceecreaaaeeeccaaeeaccaaeeaccceercrerc 180
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                       CCCCCTCCTGTGCCATCATGATCAGCACCTATGAGTTCGGCAAAAGCTTCTTCCAGAGGC
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99US-0232149.
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99US-0352616.
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2000US-0536857.
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14-JUL-1998;
23-SEP-1998;
15-JAN-1999;
09-APR-1999;
13-JUL-1999;
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09-MAY-2000;
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09-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatment of cancers, particularly prostate cancer. The present sequence is a cDNA described in the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGGGGGCTTGTTTCCCTTCCCTCCCGGCGACAAGCTCCAGGGCAGGGCTGTCCCTCTGG 1324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 CCACGGATGGGGAGAGGGCAGGAGGCCCAGCCAAGTGCCTTTTCCTCAGGACTGAGG 240
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Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1085 CCCCCTCCTGTGCCATCATGATCAGCACCTATGAGTTCGGCAAAAGCTTCTTCCAGAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCCCCTCCTGTGCCATCATGATCAGCACCTATGAGTTCGGCAAAAGCTTCTTCCAGAGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1205 CCACGGATGGGGAGAGGGCAGGAGAGGACCAAGCCAAGTGCCTTTTCCTCAGCACTGAGG
                                                                                                                                                                                                                                                                                                                                                                              New prostate-specific polynucleotides for diagnosing and treating diseases, in particular prostate cancer, and as markers for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 522; DB 24; Length 537;
Pred. No. 8.7e-119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                            Harlocker SL, Jiang Y,
A, Day CH, Vedvick TS,
apler WT, Henderson RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 537 BP; 116 A; 167 C; 138 G; 116 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33.8%; Sco...
100.0%; Pred. No. v...
... 0; Mismatches
                                                                                                                                                                                                                                                                                                         Dillon DC, Mitcham JL, Harlocker
GR, Retter MW, Stolk JA, Day CH,
Wang A, Skeiky YAW, Hepler WT,
                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 387; 87pp; English.
                                  2000US-0636215.
2000US-0651236.
2000US-0657279.
           2000US-0593793.
2000US-0605783.
                                                                   2000US-0679426.
2000US-0685166.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 522; Conservative
                                                                                                                          MITCHAM J L.
HARLOCKER S L.
                                                                                                                                                                                                                                                                                      HENDERSON R A.
                                                                                                                                                                                                                                                                                                                                                                                                     progression of cancer
                                                                                                                                                                                                                                                                SKEIKY Y A W.
HEPLER W T.
                                                                                                                                                         KALOS M D.
FANGER G R.
RETTER M W.
STOLK J A.
DAY C H.
                                                                                                                                                                                                                  VEDVICK T S.
                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-255649/30.
                                                                                                               DILLON D C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                              CARTER D.
                                                                                                                                                  JIANG Y.
                                                                                                                                                                                                                                        LI S X.
WANG A.
                                            29-AUG-2000; 2
06-SEP-2000; 2
02-OCT-2000; 2
10-OCT-2000; 2
                      27-JUN-2000;
                                 10-AUG-2000;
                                                                                                                                                                                                                                                                                                                     GR,
                                                                                                                                                (JIAN/)
(KALO/)
(FANG/)
                                                                                                                                                                                 (RETT/)
(STOL/)
(DAYC/)
                                                                                                                                                                                                                                                                         (HEPL/)
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                                                                                                                                                                                                                                                                                                                        Fanger (
Li SX,
                                                                                                                                     HARL/)
                                                                                                                                                                                                                                         LISX/)
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                                                                                                                                                                                                                                                                                                             Xu J,
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The invention relates to 625 polynucleotides which have been derived from a variety of human tissue sources and which encode novel secreted proteins, their complements and sequences that hybridise to them.

C proteins, their complements and sequences that hybridise to them.

CC transformed with the vector, comprising the polynucleotide, a host cell proteins antibodies that bind to the proteins and identification of modulators of the proteins or the expression of the polynucleotide.

CC The polynucleotides can be used as probes for the identification and isolation of full length cDNA and genomic DNA. The polynucleotides and isolation of full length cDNA and genomic DNA. The polynucleotides and proteins can also be used as nutritional supplements. The protein cut is useful in the treatment of various immune deficiencies and disorders (c.g. rheumatoid arthritis, multiple sclerosis, autoimmune disorders (e.g. rheumatoid arthritis, multiple sclerosis, conditions (e.g. asthma). They are also useful for treating neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                      Human, ss, gene, secreted protein, immune deficiency, viral infection; bacterial infection; fungal infection, autoimmune disorder; burn, rheumatoid arthritis; multiple sclerosis; autocimmune thyroiditis; Alabetes; allergy; astima, neurodegenerative disease; crohn's disease; coagulation disorder; haemophilia; inflammatory disorder; ulcer; lissue regeneration; wound healing; haematopoiesis; myeloid deficiency; lymphoid cell deficiency;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Six hundred and twenty five polynucleotides derived from a variety of human tissue sources which encode secreted proteins, useful for treating immune deficiencies and disorders such as autoimmune disorders
CTTACCCCACCCCCAAGTTCAAGACCAAATCTTCCAGCTGCCCCCTTCGTGTTTCCTGT
                                                                                                                         480
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                       GITIGCTGIAGCTGGGCATGTCTCCAGGAACCAAGAAGCCCTCAGCCTGGTGTAGTCTCC
                                                                                                         421 GTTTGCTGTAGCTGGGCATGTCTCCAGGAACCAAGAAGCCCTCAGCCTGGTGTAGTCTCC
                                                                                                                                              CTGACCCTTGTTAATTCCTTAAGTCTAAAGATGATGAACTTC 1546
                                                                                                                                                                       Human cDNA for novel secreted protein, SEQ ID 504.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fechtel K, Agostino MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 269-270; 339pp; English.
                                                                                                                                                                                                                                                                                 BP
                                                                                                                                                                                                                                                                           ABK34735 standard; cDNA; 2170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-MAR-2001; 2001WO-US10295.
                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GEMY ) GENETICS INST INC.
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K, Graham JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-179323/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200177290-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                08-MAY-2002
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                                                                                                                                                                                                                                                                                                                ABK34735;
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88888888	disease), liver fibrosis, coagulation disorders (e.g. haemophilia), inflammatory discorders (e.g. Crohn's disease) and tumours. They are also useful for tissue regeneration, for wound healing and in the treatment regulating incisions and ulcers. The proteins are also useful for regulating haematopoiesis, for treating myeloid or lymphoid cell deficiencies. The present sequence is one of the 625 cDNA sequences encoding a secreted protein.	
800	Seguence 2170 BP; 407 A; 663 C; 636 G; 460 T; 4 other;	
Mal	ery Match 33.5%; Score 517.2; DB 24; Length 2170; st Local Similarity 64.0%; Pred. No. 2e-117; tches 1290; Conservative 0; Mismatches 8; Indels 718; Gaps 5;	
S S	100 CAGGACTGAAGCTTCAAGATGGCTGACGACCCCTGCGGGGCAATCAGCCCCCTCCAGCAA 159	
à	160 ATGGTGGCCTCAGGCACCGGGGCTGTGGTTACCTCTTTCATGACACCCCTGGACGTG 219	
<u>DF.</u>	208 ATGGTGGCCTCAGGCACCGGGGCTGTGGTTACCTCTCTCT	
P 64	220 GTGAAGGTTGGCCTGCAGTCTCAGGGGCCTCCATGGCCAGGGAGCTGATGCCTTCCTCC 279	
š	80 AGACTGTGGAGCTCTCCTATACCAATGGAAGTGCCTCCTGTATTGCAATGGTGTCTG 33	
op O	328 AGACTGTGGAGCCTCTCCTATACCAATGGAAGTGCCTCCTGTATTGCAATGGTGTCCTG 387	
S G	340 GAGCCTCTGTACCTGTGCCCAAATGGTGCCGGCTGTGCCACCTGGTTTCAAGACCCTACC 399	
Oy Dp	400 CGCTTCACTGGCACCATGGATGCCTTCGTGAAGATCGTGAGGCACGAGGGCACCAGGACC 459	
85 B	460 CTCTGGAGCGSCCTCCCCGCCACCAGCTGACTGTGCCAGCTACCGCCATCTACTTC 519 -	
Q7 Q2	520 ACTGCCTATGACGAACTGAAGGCCTTCCTGTGTGGTCGAGCCCTGACCTCTGACCTCTAC 579	
ò	580 GCACCCATGGTGGCTGGCTGGCCGCC	
Д	- (°)	
8	611	
qq	688 CICIGICCCCACCICGGCCCAAACCCAGICAGICCCAGCCCCCAGCCCCCAACCICIGCCA 747	
ò	611 610	
QQ	748 GCCTAGGGATAGGGGGGTGTTCTAGGTCCCCAGACCTGGGACAGCAGGTAGGT	
δλ	611TGGGCA 616	
Db	808 TGTAAGACCTGTGATCTCACTTCTCCCCATTGTCACCCCCAATCCCCCACACAGTGGGGA 867	
ò	617 CCGTGACTGTGATCAGCCCCCTGGAGCTTATGCGGAACGTGAAGCTGACAGCATGTGT 676	
QQ	868 CCGTGACTGTGATCAGCCCCCTGGAGCTTATGCGGACAAAGCTGCAGGCTCAGGATGTGT 927	
Oy Dp	677 CGTACCGGGAGCTGGGTGCTTGGAACTGCAGTGGCTCAGGGTGGCTGGC	
à à	37 TGTGGCTGGGCTGGGGCCCCATCGAGATGTGCCCTTCTC 78	
වූ	F	

ò	783 782	0)
DP	1048 GCTGCAAGGGGTGGGTGAGGGAACCCTTGGGTGATGCACAAAGGGTCTACAGCCNANGTC 110	10
6	783	01
qu	1108 CAANTTIGIGACTAGTGACCATGAAGTTACTTAGCTTTTCTTGACCCATGGGTTTCTCAT 116	2.3
λ	783 783	01
qq	1168 CTGTGAAGTGGGCCTAGCAGGTAGAGTATTTGCCCAGNCGGTCAGAAGATTAATTCCTAC 122	7
ò	783 783	ο.
g	1228 AGAGTGCCTGCTTCTGAGCCTGCATGTAGCAGACAAAGACTCACAGCTGGGAGGGA	7.8
ò	783 783	01
QQ	1288 GGCAGTGAAAGGTGGACGGTCTGGGGCCACTTCCTTGCCCTTCCCGTCTTAATCAGTGC 134	1.3
ò	783AGCCCTGTACTGGTTCAACTGAGGCTGGTGAAGAGCTGGCTCAATG 829	•
Db	CTGIACTGGTTCAACTATGAGCTGGTGAAGAGCTGGCTCAAT	7.
ò	830 GGTTCAGGCCGAAGGACCAGACTTCTGTGGGCATGAGCTTTGTGGGCTGGTGGCATCTCAG 889	ø)
QO	rcadeccdaadeaccadactrcrerdedecardactrrrerdedredearcrea	2.7
λõ	890 GGAC	~
qq	1468 GACGCTCAGTGGACTGGGCTGAAGGTGAGGCCAGCGGAGGTCTCCCTGCGGGGGCCTG 152	7
ò	894	_
qq	1528 AGGATITITIGGAGAIGCCCAGAAGCAGACCCCATGAGGCCTITIGICCCTCCCAGCCGCAA 158	37
ò	894	
Ор	1588 GAGCCATCTGGGAGGTAGGGGGGGGGGTCCAAGAAGTGGAGCTGAGCCCTCTCCCCGCCC 164	17
δ	894GGTGGCTGCAGTGCTGACTCTACCCTTTGACGTGGTAAAGACCCAACGCCA 944	
QQ	CTGACTCTACCCTTTGACGTGGTAAAGACCCAACGCCA 17	20
δλ	945 GOTCGCTCTGGGAGCGATGGAGGCTGTGAGGGGTGAACCCCCTGCATGGGGACTCCACCTG 100	
qq	CCTCTGGGAGCGATGGAGGCTGTGAGGTGAACCCCCTGCATGTGGACTCCAC	2.3
δi	05 GCTGCTGCTGCGGAGATCCGGGCCGAGTCGGGGACTCTTTGCAGGTTCCT 10	4, 1
gg	CTGCTGCTGCGGAGGATCCGGGCCGAGTCGGGCACCAAGGGACTCTTTGCAGGCTTCCT	
& 9a	1065 TCCTCGGATCATCAAGGCTGCCCCCTCCTGTGCCATCATGATCAGCACCTATGAGTTCGG 112	37
ò	TTCTTCCAGAGGCTGAAC	34
q	1888 CAAAAGCTTCTTCCAGAGGCTGAAACCAGGACCGGCTTCTGGGCGGCTGAAAGGGCCAAGG	17
ò	1185 AGGCAAGGACCCCGTCTCTCCCAGGAGGAGA-GGGCAGGAGAGACCCAGCCAA 124	1
Dp	CGGATGGGGAGATGGGCAGGAGAGACCCAGC	7.0
Š ć	1242 GTGCTTTTCCTCAGCACTGAGGAGGGGCTTGTTTCCCTTCCCTCCC	۲ E
3	** C. C. C. C. C. C. C. C. C. C. C. C. C.	
<u> </u>	1302 CCAGGGCGGGCTCTCTCGGCGGCCCAGCACTTCTCAGAAACTCTTCTGCTGC 136	4 5
Q A	UDB CCAGGGCGGCTGTCCTCTGGGCGGCCCCAGCACTTCCTCAGACACAACTTCTTGCTGC ZI	

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TGGACTCCACCTGGCTGCTGCGGAGGATCCGGGCCGAGTCGGGCACCAAGGGACTCT 1051
                                                                                                                                                                            932 AGACCCAACGCCAGGTCGCTCTGGGAGCGATGGAGGCTGTGAGAGTGAACCCCCTGCATG 991
                                                                                                                                                                                                                                                                                                           600 CTTACGAGTTTGGCAAAAGCTTCTTCCAGAGGCTCAACCAGGAGCAGCCTCTTGGCCGCT 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes in a
                                                      181 CITCCTCTGTTCAAGCTGCGGTGACTCAGGGTGGCTGGCGCTCTCTGTGGTGGCTGGGCTGGG
                                                                                                                      241 Grecekackertreskakarerecerrerekerererkerkerrekerkerkerker
                                                                                                                                                                                                                    TGGCTGGTGGCATCTCAGGGACGGTGCTGCAGTGCTGACTCTACCCTTTTGACGTGGTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene, liver cancer, ds; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; disease st disease progression; drug toxicity; drug efficacy; drug metabolism.
                             GTGCCTGTGTTCGAACTGCAGTGGCTGAGGTGGCTGGCGCTCACTGTGGCTGGGCTGGG
                                                                                        GCCCCACTGCCCTTCGAGATGTGCCCTTCTCAGCCCTGTACTGGTTCAACTATGAGCTGG
                                                                                                                                                       TGAAGACTGGCTCAATGGGTTCAGGCCGAAGGACCAGACTTCTGTGGGCATGAGCTTTG
                                                                                                                                                                                                                                                                                                                                                                     TIGCAGGCTICCTICCTCGGAICATCAAGGCTGCCCCTCCTGTGCCATCATGATCAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                  1112 CCTATGAGTICGGCAAAAGCTICTTCCAGAGGCTGAACCAGGACCGGCTTCTGGGCGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene #1133 used to diagnose liver cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA; 452 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1172 GAAAGGGGCAAGGA 1185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      660 TGAAGTCGGGAGCA 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GENE-) GENE LOGIC INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Horne D, Alvares C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-426119/45.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABN94635 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a genes (I) in a test sample comprising genes salected from (I). The method is useful for examining the ischaemic condition (e.g. compressive schaemia, occlusive ischaemia or vasospastic ischaemia, by measuring expression levels of particular genes (AB192202 to AB19912, encoding the protein sequences in ABB57202 to ABB5734) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition.improving drugs or therapeutics for ischaemic diseases. AB19913 and AB19914

Crepresent PCR primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  512 TCTACTTCACTGCCTATGACCAACTGAAGGCCTTCCTGTGTGGTCGAGCCCTGACCTCTG 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   572 ACCTCTACGCACCCATGGTGGCTGGCGCGCTGGCCCTGGGCACCGTGACTGTGATCA 631
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                                                                                                                                                                                                                                   Mouse; ischaemia; compressive ischaemia; occlusive ischaemia; vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 ACCTCTACGCACCCATGGTGGCTGGTCCCCGCCCGAATGAG--CCGTGACAGTTGTCA
                                                                                                                                                                                                       Mouse ischaemic condition related cDNA sequence SEQ ID NO:675.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 30.4%; Score 470.4; DB 24; Length 704; al Similarity 83.1%; Pred. No. 4.8e-106; 560; Conservative 0; Mismatches 111; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 4.8e-106;
0; Mismatches 111;
1362 TGCTCCAGTCGTGGGGATCATCACTTACCCACCCC 1397
                  2128 TGCTCCAGTCGTGGGGATCATCACTACCCACCACC 2163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nagata T,
                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Page 1679-1680; 2690pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Takahashi Y,
                                                                                                         ABI99647 standard; cDNA; 704 BP.
                                                                                                                                                                                                                                                                                                                                                                               18-MAY-2001; 2001WO-JP04192.
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                                                                                                                                                                         (first entry)
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Best Local Similarity
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                                                                                                                                          ABI99647;
                                                                           RESULT 12
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                                                                The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver
                                                                                                  progression of liver cancer, hepatocellular carcinoma or metastatic liver tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN93503-ABN97455 in a tissue sample. The method of the invention has bepactoropic, and cytostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     drug toxicity, drug efficacy and drug metabolism.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCTTCCCTCCCGGCGACAGGCTCCAGGGCAGGGCTGTCCCTCTGGGCGGCCCAGCACCTTC 1339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 445.4; DB 24; Length 452; Pred. No. 5.9e-100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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Claim 1; SEQ ID NO 1133; 298pp; English.
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99.8%;
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The present invention relates to nucleic acids from the mouse, where the nucleic acid is associated with apoptosis. The sequences can be used in the diagnosis, treatment and prevention of diseases associated with excessive or inadequate apoptosis, including tumours, autoimmune diseases, viral infections, degradative diseases (Alzheimer's, Parkinson's and Huntington's diseases), repetitision injury, stroke and alcohol-induced injury to the liver, for identifying agents for treating these diseases, and to prepare transgenic animals in which expression of an apoptosis related sequence is altered. These are useful for genetic and/or pharmacological investigations of apoptosis and related diseases, another sequences of apoptosis and related diseases, another apoptosis related sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      New apoptosis-associated nucleic acid sequences and polypeptides, useful for diagnosis, treatment and prevention of e.g. tumors and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97 ccnadecaddaridaaariccaadardardarcaddaccerededdearradceeeerr
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                                                                                                                                                                                                                                                                                                         Gewies A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 6.5e-98;
0; Mismatches 123; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence 758 BP; 136 A; 244 C; 206 G; 149 T; 23 other;
                                                                                                                                                                                                                                                                                                         Cramer U,
                                                                                                                                                                                                                                              (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN
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                                                                                                                                                                                                                                                                                                      N, Braziulis E, C
Gille H, Klein M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 165; 227pp; German.
                                                                                                                  30-MAY-2001; 2001DE-1026344.
                                                                                                                                                                                   14-JUL-2000; 2000DE-1034303
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vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antiviral; antibacterial; antifungal; antihematic; antihyroid, antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia, noctuinal haemoglobinuria; burn; wound; bone damage; cartilage damage; antihlammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytostatic; hepatotropic; nootropic; neuroprotective;
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                                                                                                                                                                                                                                                        AAGATTGNGCGGCATGAGGGCACTAGGACCCTGTNNANNGGCCTCCNAGCCACCCTGGNG 516
                                                                                                                                                                                                       CTGGGCACCGTGACTGTGATCAGCCCCCTGGAGCTTATGCGGACAAAGCTGCAGGCTCAG 669
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                                                                   ATGACTGTGCCAGCTACCGCCATCTACTTCACTGCCTATGACCCAACTGAAGGCCTTCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATGTGTACCGGGAGCTGGTGCCTGTGTTCGAACTGCAGTGGCTCAGGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAC76691 standard; cDNA; 6712
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antipsoriatic, antiparkinsonian; nootropic; neuroprotective; casteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunosuppressant; antidiabetic; hypotensive; thrombolytic; coaguiant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; cantifingabetic; hypotensive; dermatological; immunosuppressive; cantifingation antianeamic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating catchins abe used to express ORX proteins in gene therapy. The proteins and mucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, conturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
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us-09-888-358-2.rng

Search completed: January 22, 2003, 19:04:05 Job time : 387.534 secs 1142 GGCTGAA 1148 2731 AACAAAA 2725 ò ò g qq

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LENGTH: 1643 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SYNOOAT01
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Sequence 68, Appl
Sequence 387, App
Sequence 387, App
Sequence 23, Appl
Sequence 262, Appl
Sequence 262, Appl
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Sequence 14, Appl
Sequence 11, Appl
Sequence 61, Appl
Sequence 11, Appl
Sequence 11, Appli
Sequence 1, Appli
Sequence 6, Appli
Sequence 9, Appli
                                                                           January 22, 2003, 16:32:11; Search time 63.3511 Seconds (without alignments) 7484.038 Million cell updates/sec
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Sequence 4, 7
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Sequence 3,
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/Patenta/1.seq:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-63-18-387

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US-09-18-930-23

US-09-188-930-23

US-09-188-930-23

US-09-188-930-24

US-09-068-140A-9

US-09-068-140A-9

US-09-068-140A-14

US-08-33-750C-61

US-08-23-463-14

US-09-24-613-61

US-09-24-613-61

US-09-34-613-61

US-09-34-613-61

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US-09-34-75-4

US-09-24-75-4

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Maximum Match 100%
Listing first 45 summaries
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Sequence 1, Appli
Sequence 43, Appl
Sequence 1, Appli
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Sequence 1, Appli
Sequence 48, Appl
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Sequence 1
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Sequence 1
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APPLICANT: Bandman, Organ
APPLICANT: Shah, Purvi
APPLICANT: Au-Young, Janice
APPLICANT: Vue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Gorley, Neil C.
APPLICANT: Gorley, Neil C.
MUMBER OF SEQUENCES: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: DISACTORE
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FESTESCY for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750C
FLING DATE: September 23, 1997
CLASSIFICATION NUMBER: US/08/933,750C
FLING DATE: APPLICATION DATA:
FILING DATE: APPLICATION DATA:
APPLICATION NUMBER: SILING DATE: ATORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: PF-0356 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
              US-08-379-452-43

US-09-244-752-1

US-09-244-752-1

US-09-245-497-1

US-09-65-919-1

US-08-62-919-1

US-08-62-919-1

US-08-62-919-1

US-08-98-416-471

US-08-98-416-471

US-08-99-227-10

US-08-99-227-10

US-09-244-332-3

US-09-385-028-13

US-09-385-028-13

US-09-385-028-13

US-09-385-028-13

US-09-385-028-13

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US-09-385-028-13
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STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                         %30-08-933-750C-68
; Sequence 68, Application US/08933750C
; Patent No. 5932442
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTR. 219. 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
TYPE: IBM Compatible
TYPE: IBM Compatible
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ADDRESSEE: Incyte Ph
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GENERAL INFORMATION:
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TELEFAX: 415-845-4166

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1147 ITCCTTCCTCGGATCATCAAGGCTGCCCCTCCTGTGCCATCATGATCAGCACCTATGAG 1206
                                                         1207 TTCGGCAAAACTTCTTCCAGAGGCTGAACCAGGACCGGCTTCTGGGCGGCTGAAAGGG 1266
                                                                                              CAAGGAGGCAAGGACCCCGTCTCCCACGGATGGGGAAGGGGCAGGAGGAGAACCCAGCC 1239
                                                                                                                       AAGTGCCTTTTCCTCAGCACTGAGGAGGGGGCTTGTTTCCCTTCCCTCCGGGGACAAG 1299
                                                                                                                                                                                 CTCCAGGGCAGGCTGTCCCTCTGGGCGGCCCAGCACTTCCTCAGACACAACTTCTTCCT 1359
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                                     TTCGGCAAAAGCTTCTTCCAGAGGCTGAACCAGGACCGGCTTCTGGGCGGCTGAAAGGGG
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APPLICANT: Hilman, Jemnifer L.
APPLICANT: Alliman, Jemnifer L.
APPLICANT: Shah, Purvi
APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Yue, Henry
APPLICANT: Ociley, Nail C.
TITLE OF INVENTION: HOWAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FASTSEO for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/234,613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0356 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Incyte Pharmaceuticals,
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US-09-234-613-68
Sequence 68, Application US/09234613
Patent No. 613.973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRICE APPLICATION DATA:
APPLICATION NUMBER: US/08/933,
FILING DATE: September 23, 199
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3174 Porter Drive
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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CITY: Palo Alto
STATE: CA
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                                                                                                                                                                  219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCTGGAGCGGCCTCCCCGCCACCTGGTGATGACTGTGCCAGCTACCGCCATCTATC 606
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                                                                                                                                                          ATGGTGGCCTCAGGCACCGGGGCTGTGGTTACCTCTCTTCATGACACCCCTGGACGTG
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                                             Length 1643;
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                                           DB 2;
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                                    93.4%; Score 1732...
99.9%; Pred. No. 0;
                                                      Best Local Similarity 99.9
Matches 1445; Conservative
, CLONE: 724157
US-08-933-750C-68
                                           Query Match
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                                                                  1027 CGCCAGGTCGCTCTGGGAGCGATGGAGGCTCTGAGAGTGAACCCCCTGCATGTGGACTCC
                                                                                                  ACCTGGCTGCTGCTGCGGAGGATCCGGGCCGAGTCGGGCACCCAAGGGACTCTTTGCAGGC
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APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C16
CURRENT APPLICATION NUMBER: US/09/605,785
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Patent No. 6321716
GENERAL INFORMATION:
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Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Stolk, John A.
Bay, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
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                                                                                                                                                                                                                                     Length 1643;
                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                   DB 3;
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                                                                                                                                                                                                                                             Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                  Score 1443.8;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                      INFORMATION FOR SEQ ID NO: 68: SEQUENCE CHARACTERISTICS: LENGTH: 1643 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear IMMEDIATE SOURCE:
                                                               68:
                                                                                                                                                                                                                                93.4%;
                                                                                                                                                                                                                                           Best Local Similarity 99.9
Matches 1445; Conservative
                                                                                                                                                                LIBRARY: SYNOOAT01
CLONE: 724157
                                                                                                                                                                                                US-09-234-613-68
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1419

SEQ ID NO 387

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APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Harlocker, Susan Louise
APPLICANT: Galos, Michael
APPLICANT: Galos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Setter, Mark
APPLICANT: Solk, John
APPLICANT: Bolk, John
APPLICANT: Day, Craig
ITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
ITLE OF INVENTION: DIAGNOSITIONS OF PROSTATE CANCER
FILE REFERENCE: 210121.42709
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILICATION NOWS: 575
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                   Length 537;
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                                                                                                                                                                                            Query Match 33.8%; Score 522; DB 4; Le Best Local Similarity 100.0%; Pred. No. 1.1e-126; Matches 522; Conservative 0; Mismatches 0;
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 387, Application US/09439313 Patent No. 6329505
                                                                                                          TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                    US-09-605-785-387
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                                                                                        LENGTH: 537
                                                                SEQ ID NO 387
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Fatent No. 6395278
GENERAL INDERMATION
FARENCE TO BOXIN C.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang Yuqui
APPLICANT: Micham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 21021,427C8
CURRENT BILING DATE: 1999-07-13
NUMBER OF SEQ ID NOS: 472
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                          61 CCCCTCCTGTGCCATCATGATCAGCACTATGAGTTCGGCAAAAGCTTCTTCCAGAGGC
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                                                                            Query Match
33.8%; Score 522; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 1.1e-126;
Matches 522; Conservative 0; Mismatches 0;
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33.8%; Score 522; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 1.1e-126;
Matches 522; Conservative 0; Mismatches 0;
                   ORGANISM: Homo sapiens
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CRCANISM: Homo sapiens
US-09-352-616A-387
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US-09-352-616A-387
                                        US-09-439-313-387
TYPE: DNA
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ORGANISM: Mouse
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                                                                                                      61 CCCCTCCTGTGCCATCATGACTCAGCTTCGGCAAAAGCTTCTTCCAGAGGC
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Patent No. 6150502

GENERAL INDRAMATION:
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Matthew
APPLICANT: Steeman, Matthew
APPLICANT: Steeman, Matthew
APPLICANT: Only Research, Matchew
APPLICANT: Minison, James Greg
TE OF INVENTION: Compositions Isolated From Skin Cells
FILE REPERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A

CURRENT FILING DATE: 1998-11-09

NUMBER OF SEQ ID NOS: 348

SOFTWARE: PastSEQ for Windows Version 3.0
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Matches 136; Conser
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; ORGANISM: mouse
US-09-188-930-23
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US-09-188-930-23
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                                                                                                      573 CCTCTACGCACCCATGGTGGCTGGCGCGCTGGCCCGCCTGGGCACCGTGACTGTGATCAG 632
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APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Onrust, Rene
TILLE OF INVENTION: Compositions Isolated From Skin Cells
TILLE OF INVENTION: and Methods For Their Use
TILLE REFERENCE: 11000.1011c1
CURRENT FILMS DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1816;
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Patent No. 6281409
GENERAL INFORMATION:
APPLICANT: MATY Rose Woodhead, Mark Andrew Taylor
APPLICANT: and Rex Michael Brennan
TITLE OF INVENTION: Blackcurrant Promoters and Genes
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 125;
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Pred. No. 1.4e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 262, Application US/09188930A
Patent No. 6150502
                                                                                                                                                                                                                                                         958 CCCAATGGAGGTTCTGAAGAC 978
                                                                                                                                                                                                                         CCCCCTGGAGCTTATGCGGAC 653
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us-09-888-358-2.rni

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NAME: Dinner, Dara L.
REGISTRATION NUMBER: 33,680
REBERNCE/DOCKET NUMBER: C702.
TELECOMMUNICATION INFORMATION:
TELEPROME: 610-270-5017
TELEPROME: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA (genomic)
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SEQUENCE CHARACTERISTICS:
LENGTH: 5150 base pairs
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CLASSIFICATION:
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STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                     US-09-068-140A-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       458 CCCTCTGGAGGGCCTCCCCGCCACCCTGGTGATGACTGTGCCCAGCTACCGCCATCTACT 517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       518 TCACTGCCTATGACCAACTGAAGGCCTTCCTGTGTGGTGGAGCCCTGACCTCTGACCTCT 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           326 TCTCCGTTTACGAGATGTGTAAGGAGACTTTTTCTCATGGTGATCCGAGC---AATTCCG 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      578 ACGCACCCATGGTGGCTGGCGCGCTGGCCCCGCTGGCCACCGTGACTGTGATCAGCCCCC 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            443 TGGATGTGGTGAAACAGAGGTTGCAGATGCAGAGCAGTCCGTACAAGGGTGTTGTTGATT 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       698 GTGTTCGAACTGCAGTGGCTCAGGGTGGCTGGCGCTCACTGTGGCTGGGCTGGGGCCCCA 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        758 CIGCCCTTCGAGAIGTGCCCTTCTCAGCCCTGTACTGGTTCAACTATGAGCTGGTGAAGA 817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        398 CCCGCTTCACTGGCACCATGGATGCCTTCGTGAAGATCGTGAGGCACGAGGGCACCAGGA 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             383 GTGCGCACGCCGTTTCGGGGGTGTTCGCGACGTGGAGGGACGACGCGGTGATTACGCCGA 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     503 GCGTGAGGAGGAGGTGTTGGTAGAAGAAGGGATTGGCGCATTTTACGCATCTTATCGAACAA 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               563 CTGTGGTCATGAATGCCCCCGTTTACGGCCGTTCACTTCGCCACATATGAAGCCCACGAAGA 622
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 623 AAGGGTTGTTGGAGGTGTCGCCGGAGACTGCGAACGATGAGAATTTGTTAGTGCATGCTA 682
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                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
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3.2%; Score 48.8;
Best Local Similarity 45.7%; Pred. No. 0.0
                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/04807
FILING DATE: NO. 6281499ember 4, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                         APPLICATION NUMBER: US/09/068,140A
                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                             C70237
                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 33,680
REFERENCE/DOCKET NUMBER: C7023
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5090
TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1311 base pairs
                                                         ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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King of Prussia
PA
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EDNESS: unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
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MOLECULE TYPE: CD
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                                                                                                                                                                                                                               FILING DATE
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                                               COUNTRY:
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872 TGGCTGGTGGCATCTCAGGGACGGTGGCTGCTGCTGACTCTACCCTTTGACGTGGTAA 931
                                                        683 CTGCTGCTGCTGCTGCTGCTTTGCTGCTGCAGTAGTAACCACTCCACTAGATGTTGTCA 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3430 GACTTTACCGTGGCATTGGTGCAATGGGTCTCGGTGCAGGACCAGGTCACGCAGTGTATT 3489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
WEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORPUTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
APPLICATION NUMBER: US/09/068,140A
                                                                                                                                                                                                                                                                                                                                                                     Sequence 14, Application US/09068140A
Patent No. 6281409
GENERAL INFORMATY
APPLICANT: Mary Rose Woodhead, Mark Andrew Taylor
APPLICANT: and Rex Michael Brennan
TILLE OF INVENTION: Blackcurrant Promoters and Genes
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEE: SmithKline Beecham Corporation
: 709 Swedeland Road
King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/04807
FILING DATE: No. 6281409ember 4, 1996
ATTORNEY/AGENT INPORMATION:
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                3490 rcrccarriacaagargrgraagacrriricrcargarcaaccaac---aarrccg 3546
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                                                                                                3547 Grácica coccintros de controdos de como conocio de contra con como 3606
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                                                          578 ACGCACCCATGGTGGCTGGCGCGCTGGCCCGCCTGGGCACCGTGACTGTGATCAGCCCCC 637
                                                                                                                                                                                                                                                                                                                                                                                  818 GCTGGCTCAATGGGTTCAGGCCGAA----GGACCAGACTTCTGTGGGGCATGAGCTTTG 871
                                                                                                                                                                                                                      638 TGGAGCTTATGCGGACAAAGCTGCAGGCTCAGCATGTGTGTCGTACCGGGAGCTGGGTGCCT
SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: DORNER, F.
APPLICANT: SCHEFLINGER, F.
APPLICANT: FALKUER, F. G.
APPLICANT: FALKUER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLFOX VIRUS
NUMBER OF SEQUENCES: 52
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ADDRESSES: FOLEY & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
NTTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
FILING DATE:
FILING DATE:
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 14, Application US/08232463; Patent No. 5670367; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29,768
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FELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (703)683-4109
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3907 AAACTCAGTTGCAG 3920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              932 AGACCCAACGCCAG 945
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US-08-232-463-14
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TELEX: 8
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                                                                                                                                                                                                                                                        1381 ATCACTTACCCACCCCCCAAGTICAAGACCAAATCTTCCAGCTGCCCCCTTCGTGTTTCC 1440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                   h 2.8%; Score 43.2; DB 1; Length 7218; Similarity 3.4%; Pred. No. 0.1; 9; Conservative 156; Mismatches 99; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: HUMAN REGULATORY MOLECULES NUMBER OF SEQUENCES: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Incyte Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0356 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1292 YYYYYYYYYYYYYYYYYYY 1315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1501 CTCCCTGACCCTTGTTAATTCCTT 1524
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Patent No. 5932442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: September 23, 1997
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Hillman, Jennifer L.
Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Au-Young, Janice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yue, Henry
Guegler, Karl J.
Corley, Neil C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 3174 Porter Drive CITY: Palo Alto STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
7218 base pairs
               TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                 ; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F1s
US-08-232-463-14
                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-933-750C-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                        Matches
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RESULT 13
US-08-961-871-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1061 CCACAGGCTTCATGTTCTTCTCGTATGATTCTTCTGTAATGTCTTCCACCTGCATGAAC 1119
                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                          Query Match 2.7%; Score 42.2; DB 2; Length 1594; Best Local Similarity 59.7%; Pred. No. 0.11; Matches 71; Conservative 0; Mismatches 48; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Shah, Purvi
APPLICANT: Yue, Henry
APPLICANT: Osegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/COCKET NUMBER: PF-0356 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFRAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750
FILING DATE: September 23, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 61, Application US/09234613 Patent No. 6132973
                                   INFORMATION FOR SEQ ID NO: 61.
SEQUENCE CHARACTERISTICS.
LENGTH. 1594 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Facet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX:
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H: 1594 base pairs
nucleic acid
DEDNESS: single
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                       LIBRARY: SPLNNOT02;
CLONE: 207452
US-08-933-750C-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-234-613-61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY:
STATE:
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                                                                                                                                                                                                                                                                                   1001 AGGAAGGCCCTGGGCTTCTTCAAGGCCTGTCCCCCAGCTTGCTGAAGGCTGCCTCT 1060
                                                                                                                                                                                                                                                                                                                                   1091 CCTGTGCCATCATGATCAGCACCTATGAGTTCGGCAAAAGCTTCTTCCAGAGGCTGAAC 1149
                                                                                                                                                                                                                                                                                                                                                                      1061 CCACAGGCTTCATGTTCTTCTGTATGAATTCTTCTGTAATGTCTTCCACTGCATGAAC 1119
                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11, Application US/08961871
Patent No. 6013858
PAPLICANT: Wallace, Douglas C.
APPLICANT: Wallace, Douglas C.
APPLICANT: MacGregor, Grant R.
TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine
TITLE OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                       Query Match 2.7%; Score 42.2; DB 3; Length 1594; Best Local Similarity 59.7%; Pred. No. 0.11, Matches 71; Conservative 0; Mismatches 48; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.6%; Score 40.8; DB 3; Length 1259; Best Local Similarity 50.0%; Pred. No. 0.22; Matches 102; Conservative 0; Mismatches 102; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 31-OCT-1997
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Greenlee, Winner and Sullivan, P.C. STREET: 5370 Manhattan Circle, Suite 201 (EITY: Boulder STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/030,017
FILING DATE: 01-NOV-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33,878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (303) 499-8089
INPORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1259 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             not relevant
E: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Ferber, Donna M. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                190..1086
                                          ; LIBRARY: SPLNNOT02
; CLONE: 207452
US-09-234-613-61
TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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1033 TCCTTTTTGCGTTTGGGATCCTGGAACGTGGTGATGTTCGTAACCTATGAGCAGCTGAA 1091
                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 6
LENGTH: 897
                                                                     RESULT 15
US-09-434-288-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-434-288-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM:
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403 ITCACTGGCACCATGGATGCCTTCGTGAAGATCGTGAGGCCACGAGGGCACCAGGACCCTC 462
                                      340 TACAAAGGCATCATTGATTGTGTCGTGAGAATCCCCAAGGAGCAGGGCTTTCTCTCTTTC 399
                                                                                         522
                                                                                                                      400 TGGAGGGGTAACCTGGCCAACGTGATCCGGTACTTCCCCACTCAAGCCCTGAACTTCGCC 459
                                                                                                                                                                   523 GCCTATGACCAACTGAAGGCCTTCCTGTGTGGTGGAGCCCTGACCTCTGACCTCTACGCA 582
                                                                                                                                                                                                           460 TTCAAAGACAAGTACAAGCAGATCTTCCTGGGAGGCGTGGATCGCCATAAGCAGTTCTGG 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  973 İGİAİGALAAAGATGGİĞĞÇÇĞAĞĞĞĞĞÇÇÇAKGĞÇTİÇİAÇAAĞĞATTTACAÇÇ 1032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          403 TICACTGGCACCATGGGTGCCTTCGTGAAGATCGTGAGGCACGAGGGCACCAGGACCCTC 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                673 TACAGCGGGACTATGGACGCCTACAGAACCATCGCCAGGAGGAGGAGAGGAGTCAGGGCCTG 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             463 IGGAGGGGCCTCCCCGGCCACCCTGGTGATGACTGTGCCAGCTACCGCCATCTACTTCACT 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        793 ACCTACGACATCCTCAAGGAGAAGCTGCTGGACTACCACCTGCTCACTGACAACTTCCCC 852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     733 TGGAAAGGAACTTTGCCCAACATCATGAGGAATGCTATCGTCAACTGTGTGAGGGGGGTG 792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  583 ---CCCATGGTGGCTGGCGCGCTGGGCACCGTGACTGTGATCAGCCCCTG 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             853 IGCCACTITIGICTICIGCCTTIGGAGCCGCCTICTGIGCCACAGIGGTGGCCTCCCCGGTG 912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   640 GAGCTTATGCGGACAAAGC---TGCAGGCTCAGCATGTGTCGTACCGGGAGCTGGGTGCC 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               913 GACGTGGTGAAGACCCGGTATATGAACTCACCTCCAGGCCAGTACTTCAGCCCCCCCGAC 972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        697 IGIGITICGAACIGCAGIGGCICAGGGIGGCIGGCGCTCACIGIGGCTIGGGCTGGGGCCCC 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               757 ACTGCCCTTCGAGARGTGCCCTTCTCGAGCCCTGTACTGATTCAACTATGAGCTGGAGA 815
                                                                                  463 IGGAGCGCCTCCCCGCCACCCTGGTGATGACTGTGCCAGCTACCGCCATCTACTTCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               523 GCCTATGACCAACTGAAGGCCTTCCTGTGGTCGAGCCCTGACCTCTGACCTTTAGGCA
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Pred. No. 0.4;
0; Mismatches 217; Indels
                                                                                                                                                                                                                                                                                                                                                                                                CURRENT FILING DATE: 1997-03-18

REALIER PILICANT: Lee James Beeley
APPLICANT: Rebert James
APPLICANT: Robert James
APPLICANT: Robert James
APPLICANT: Robert James
APPLICANT: Robert James
APPLICANT: Robert James
APPLICANT: Robert James
CURRENT APPLICATION NUMBER: US/09/142,565A
CURRENT APPLICATION NUMBER: 9704551.2
EARLIER PILING DATE: 1999-06-30
EARLIER APPLICATION NUMBER: 9705614.7
EARLIER FILING DATE: 1997-03-18
EARLIER FILING DATE: 1997-03-18
EARLIER FILING DATE: 1997-03-18
EARLIER FILING DATE: 1997-07-16
NUMBER OF SEQ ID NOS: 6
SOPTHARE: FLING DATE: 1997-07-16
NUMBER OF SEQ ID NOS: 6
SOFTHARE: FASTESEQ FOR Windows Version 3.0
                                                                                                                                                                                                                                                        583 CCCATGGTGGCTGGCGCTGGCC 606
                                                                                                                                                                                                                                                                                                  CGCTACTTTGCTGGTAACCTGGCC 543
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Best Local Similarity 46.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 196; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1192
                                                                                                                                                                                                                                                                                                                                                            RESULT 14
US-09-142-565-1
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LENGTH: 11
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Sequence 6, Application US/09434288
| Patent No. 6303767 |
| GENERAL INFORMATION: A Patent No. 6303767 |
| APPLICANT: Betlach C., Melanie |
| APPLICANT: McDaniel Robert |
| TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES AND RECOMBINANT DNA TITLE OF INVENTION: CONSTRUCTS THEREFOR |
| TITLE OF INVENTION: CONSTRUCTS THEREFOR |
| TITLE OF INVENTION: CONSTRUCTS THEREFOR |
| CURRENT APPLICATION NUMBER: US/09/434,288 |
| CURRENT FILING DATE: 1998-11-05 |
| PRIOR APPLICATION NUMBER: 60/107,093 |
| NUMBER OF SEQ ID NOS: 12 |
| SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  451 ACCAGGACCCTCTGGAGCGGCCTCCCCGCCACCTGGTGATGACTGTGCCAGCTACCGCC 510
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Published Applications NA:\*

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Sequence 46, Appl Sequence 329, Appl Sequence 2543, Ap Sequence 11674, A Sequence 288, Appl Sequence 288, Appl Sequence 387, App Sequence 387, App Sequence 1133, App Sequence 1179, App Sequence 1179, App Sequence 4486, App Sequence 1, Appli Sequence 387, App Sequence 387, App Sequence 387, App Sequence 387, App Sequence 2, Appl. Sequence 68, App Description 0 US-09-888-358-2 0 US-09-840-787-68 0 US-09-888-358-1 US-09-895-733-387 US-09-895-733-387 US-09-895-733-387 US-09-780-669-387 US-09-780-669-387 US-09-880-107-1133 US-09-867-701-4486 US-09-867-701-4486 US-09-917-800A-329 US-09-960-352-5543 US-09-864-761-11674 US-09-986-758-11708 US-09-986-761-11708 US-09-986-761-11708 US-09-986-761-11708 US-09-986-761-11708 US-09-986-761-11708 US-09-986-761-11708 US-09-986-761-11708 SUMMARIES % Query Match Length DB 00000000000 452 496 3334 3334 Score 522 522 522 622 622 722 722 118.4 185.8 170.2 17 1546 1443.8 1054.4 No. Result 

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                                  ; Sequence 2, Application US/0988358; Patent No. US20020119137A1; Patent No. US20020119137A1; GENRRAL INFORMATION:
; APPLICANT: LEWIN, DAVID
; APPLICANT: ADAMS, SEAN H.
; APPLICANT: ADAMS, SEAN H.
; TITLE OF INVENTION: CGI-69 COMPOSITIONS AND METHODS OF USE; TITLE REFERENCE: 10716/66; CURRENT APPLICATION NUMBER: US/09/888,358; CURRENT APPLICATION NUMBER: 66/213,307; PRIOR PILING DATE: 2001-06-22; PRIOR PILING DATE: 2000-06-22; NUMBER OF SEQ ID NOS: 18
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ilaxity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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241 CAGGGCCCTCCATGGCCAGGGGCTGATGCCTTCCTCCAGACTGTGGAGCCTCTCCTAT 300	301 361 361	421 GCCTTCGTGAAGATCGTGAGGCACCAGGACCCTCTGGAGCGGCCTCCCGCC	481 ACCCTGGTGATGACTGCCGCCATCTACTTCACTGCCTATGACCAACTGAAG 540	541 GCCTTCCTGTGTGGTCGAGCCCTGACCTCTACCTCTACCCCATGGTGGCTGGC	601 CTGGCCGCCTGGGCACCGTGACTGTGATCAGCCCCTGGAGCTTATGCGGACAAAGCTG 660	661 CAGGCTCAGCATGTGTCGTACCGGGAGCTGGGTGTTTCGAACTGCAGTGGCTCAG 720	721 GGTGGCTGGCGCTCACTGTGGCTGGGCTGGGGCCCCACTGCACTTCGAGATGTGCCCTTC 780	781 TCAGCCCTGTACTGGTTCAACTATGAGCTGGTGAAGAGCTGGCTCAATGGGTTCAGGCCG 840	841 AAGGACCAGACTTCTGTGGGCATGAGCTTTGTGGCTGGCATCTCAGGACGGTGGCT 900	901 GCAGIGCTGACTCTACCCTTICACGIGGTAAAACCCCAACGCCAGGICGCTCGGGAGCG 960 	961 AIGGAGGCIGTGAGAGIGAACCCCCTGCATGTGGACTCCACCTGGCTGCTGCTGCTGCGGAGG 1020	1021 ATCCGGGCCGAGTCGGGCACAAAGGAACTCTTTGCAGGCTTCCTTC	1081 GCTGCCCCTCCTGTGCCATCATGATCAGCACCTATGAGTTCGCCAAAAGCTTCTTCCAG 1140	1141 AGGCTGAACCAGGACCGGCTTCTGGGCGGCTGAAAGGGGCAAGGAGGAAGGA	1201 TCTCCCACGATGOGAGAGGAGAGAGACCCAGCCAAGTGCCTTTTCCTCAGCACT 1260 1201 TCTCCCACGATGGGGAGAGGCAGAGAGACCCAGCCAAGTGCCTTTTCCTCAGCACT 1260	1261   GAGGGGGGGTTGTTTCCCTTCCCTCCGGCGACAAGCTCCAGGGCTGTCCCT   1320	CTGGGCGGCCCAGCACTTCCTCAGACAACTTCTTCCTGCTGCTCCAGTCGTGGGGGATC
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1567 AAGCCCTCAGCCTGGTGTAGTCTCCCTGACCCTTGTTAATTCCTTAAGTCTAAAGATGAT 1626
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CAAGGAGGCAAGGACCCCGTCTCTCCCACGGATGGGGAGAGGGCAGGAGGAAAACCCAGCC
                                                                                                                                                                                                              1387 CTCCAGGGCAGGGCTGTCCCTCTGGGCGCCCAGCACTTCCTCAGACACTTCTTCCT
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APPLICANT: LEMIN, DAVID
APPLICANT: ADAMS, SEAN H.
APPLICANT: YU, XING XIBA
ITILE OF INVENTION: CGI-69 COMPOSITIONS AND METHODS OF USE
FILE REPRENCE: 10716/66
CURRENT APPLICATION UNMER: US/09/888,358
CURRENT ELLING DATE: 2001-06-22
PRIOR PILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN VEY: 2.1
SEQ ID NO
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Best Local Simi
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241 GTATTGCAATGGTGCTCCTGGAGCCTCTGTACCTGTGCCCAAATGGTGCCCGCTGTGCCAC 300
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Publication No. US20020183251A1
GENERAL INFORMATION:
APPLICANT: Mitchen, Davin C.
APPLICANT: Mitchen, Jennifer L.
APPLICANT: Harlocker, Jennifer L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Jiang, Yuqiu
APPLICANT: Stalos, Michael D.
APPLICANT: Retter, March
APPLICANT: Stolk, John A.
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Stolk, John A.
Day, Craig H.
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100.0%; Pred. No. 4.7e-131;
tive 0; Mismatches 0;
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McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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                                                                    Wang, Aijun
Skeiky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
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Best Local Similarity 100.0
Matches 522, Conservative
    Thomas
                        Carter, Darrick
Li, Samuel X.
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ORGANISM: Homo sapiens
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Vedvick,
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.477026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.8%; Score 522; DB 9; Length 537;
100.0%; Pred. No. 4.7e-131;
Live 0; Mismatches 0; Indels
CTGACCCTTGTTAATTCCTTAAGTCTAAAGATGATGAACTTC 522
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Vinals de Bassols, Carlota
                                                                                                                          Sequence 387, Application US/09895814 Publication No. US20020193296A1 GENERAL INFORMATION:
                                                                                                                                                                                       APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
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McNeill, Patricia D.
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Hepler, William T.
Henderson, Robert A.
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Vedvick, Thomas S.
Carter, Darrick
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ORGANISM: Homo sapiens
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APPLICANT: McMeill, Patricia D.
PLICANT: McMeill, Patricia D.
PLICANT: Houghton, Raymond L.
LICANT: Vinals de Bassols, Carlota
....PLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.534C2
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 387
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Skeiky, Yasir A.W.
Skeiky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
Hural, John
McWeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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Jiang, Yuqiu
Kalos Michael D.
Stelk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel X.
                        Xu, Jiangchun
Dillon, Davin C.
Mitcham, Jennifer L.
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Matches 522; Conservative
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ORGANISM: Homo sapiens
    INFORMATION:
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Db   301 GGGGCCCAGCACTTCCTCAGA   Qy   1385 CTTACCCACCCCCCAGGTTCA   Db   361 CTTACCCACCCCCCAGGTTCA   Qy   1445 GTTTCCTGTAGCTGGGGCATGT   Db   421 GTTTCCTGTAGCTGGGCATGT   Qy   1505 CTGACCTGTAGCTGGGCATGT   Q   1505 CTGACCTTGTTAANTCCTTA	481 481 481 481 590-780 590-780 590-780 590-780 4811CA APPLICA	SCRTWARE: FastSED for Windo   SED ID NO 387
	BESULT 7  US-09-759-143-387  Sequence 387, Application US/09759143  Sequence 387, Application US/09759143  Sequence 387, Application US/09759143  FERENT NO. USZ0220248A1  APPLICANT: Dillon, Davin C.  APPLICANT: Mitcham, Jennifer L.  APPLICANT: Harlocker, Susan L.  APPLICANT: Harlocker, Susan L.  APPLICANT: Harlocker, Susan L.  APPLICANT: Fanger, Gary R.  APPLICANT: Rales, Michael D. APPLICANT: Stock, John A.  APPLICANT: Stock, John A.  APPLICANT: Stock, John A.  APPLICANT: Stock, Yasir A.  APPLICANT: Stock, Yasir A.  APPLICANT: Skelky, Yasir A.  APPLICANT: Skelky, Yasir A.W.  APPLICANT: Skelky, Yasir A.W.  APPLICANT: Hapler, William  APPLICANT: Hapler, William  TITLE OF INVENTION: DIGNOSIS OF PROSTATE CANCER  FILE REFERENCE: 21012.1427023  CURRENT FILING DARE: 2010-10-12  NUMBER OF SEQ ID NOS: 9387  LENGTH: 537  LENGTH: 537  CURRENT HOM SAIPHER  CORRANTISH: Home sapiens  US-09-759-14-387	Query Match         33.8%; Score 522; DB 10; Length 537;           Best Local Similarity 100.0%; Pred. No. 4.7e-131;         Antiches 522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;           Oy 1025 GGSCCGAGTCGSCACCAAGGACTCTTTGCAGGCTTCCTTCCTCGGATCATCAAGGCT 1084         Db         1 GGGCCGAGTCGAGGACTCTTTGCAGGCTTCCTTCCTCGGATCATCAAGGCT 0184           Oy 1085 CCCCTCTGTGCCATCATGAGTCTTGCAGGATCATCAAGGCT 020         Oy 1085 CCCCTCTGTGCCATCATGAGTCAGGACTCTTTCGCAAAGGTTCTTCCAGAGGC 120           Oy 1085 CCCCTCTGTGCCATCATGAGTCAGGACTCTTTCGCAAAGGTTCTTCCAGAGGC 120         Oy 1145 TGAACCAGGACTTCTGGCGCTTCTAGAGTTCGGCAAAGGTTCTTTCCTCAGAGGC 120           Oy 1145 TGAACCAGGACGCATCTTGGCGCTTCTAGAGTTCGCAAAGGTCCTTTTTCTTCCAGAGGC 120         Oy 1205 CCACGGACGGCGCTTCTGGGCGCTGAAAGGGCAAAGGAGGCACCCGTCTTT 180           Oy 1205 CCACGGATGGGGCTTCTTGGGCGCTCAAAGGAGGCAAAGGACCCGTCTTTTCCTCAGCACTGAGG 240           Oy 1205 CCACGGATGGGGGAGAGACCCCAGCCAAAGTGCCTTTTCCTCAGCACTGAGG 240           Oy 1205 CCACGGATGGGGGAGAGGACCCCAGGCCAAAGTGCCTTTTCCTCAGCACTGAGG 240           Oy 1205 CACGGATGGGGAGAGGACCCCAGGCCAAAGTGCCTTTTCCTCAGGACTGAGG 240           Oy 1205 CACGGATGGGGAGAGGAGAGCCCCAAAGTGCCTTTTCCTCAGGACTGAGG 240           Oy 1205 GAGGGGCTTGTTTCCCTTCCCTCCCGGCCCAAAGTGCCTTTTCCTCTGG 330           Oy 1205 GAGGGGCTTGTTTCCCTTCCTCCCGGCACAAGGCTCTTTCCTCTGG 330           Oy 1325 GCGCCCACACACACACACACACACACACACACACACACA

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Query Match
Best Local Similarity 99.8
Matches 446; Conservative
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US-09-880-107-1133/c
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LENGTH: 452
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GAGGGGGCTTGTTTCCCTTCCCTCCGGCGACAAGCTCCAGGGCAGGGCTGTCCCTCTGG 1324
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Pred. No. 4.7e-131;
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                                                                                                                                                                                                                                        CTGACCCTTGTTAATTCCTTAAGTCTAAAGATGATGAACTTC 522
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REPERBENCE: 21012.53401
CURRENT APPLICATION NUMBER: US/09/822,827
CURRENT PAPLICATION NUMBER: 2001.03-28
NUMBER: FSEQ ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 337
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100.0%; Pred. No. a...
0; Mismatches
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Patent No. US20020081680A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 522; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
) ORGANISM: Homo sapiens
US-09-822-827-387
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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GITTGCTGTAGCTGGGCATGTCTCCAGGAACCAAGAAGCCCTCAGCGTGGTGTAGTCTCCC 480
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APPLICANT: Horne, Joseph G.
APPLICANT: Wockley, Joseph G.
APPLICANT: Scherf, Unc.
APPLICANT: Scherf, Unc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer, TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer, TITLE REPRENCE: 44921-5028-00;
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT PILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/231,339
PRIOR PILING DATE: 2000-06-14
PRIOR PILING DATE: 2000-06-14
PRIOR PILING DATE: 2000-06-14
PRIOR PILING DATE: 2000-06-14
NUMBER OF SEC 10 NOS: 3950
SOFTWARE: PatentIn Ver. 2.1
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Pred. No. 1.8e-110;
0; Mismatches 1; Indels
                                                                                                                                             481 CIGACCCITGITAATICCITAAGICTAAAGATGAIGAACTIC
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US-09-880-107-1179
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Best Local Similarity 97.1%; Pred. No. 1.6e-49;
Matches 233; Conservative 0; Mismatches 6; Indels 1;
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APPLICANT: Adjate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.497
CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                               APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REPERENCE: 44921-5028-WO
                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION WIMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 1179
LENGTH: 240
             Sequence 1179, Application US/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Horne, Darci T.
APPLICANT: Scherf, Uwe
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Parent No. US20020132237A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Homo sapiens
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Best Local Similarity
US-09-880-107-1179/c
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LENGTH: 453
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290 CITATGCGGACAAAGCTGCAGCATCTAGCATGTCTCGTACCGGGAGCTGGGTGCCTGTGTT 349
230 CCCATTGTCACCCCCAAATCCCCACACAGTGGGCACCGTGATCAGCCCCCTGGAG 289
                                                                                                                                                                                                                                                                                                                             350 CGAACTGCAGTGGCTCAGGGTGGCTGGCGCTCACTGTGGCTGGGGCTGGGG-CCCACTGCC 408
                                                                                                                643 CTTATGCGGACAAAGCTGCAGGCTCAGCATGTGTGTCGTACCGGGAGCTGGGTGCCTGTGTT 702
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CURRENT APPLICATION NUMBER: US/09/908,711
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US01/01360
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PRIOR FILING DATE: 2001-01-17
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PRIOR APPLICATION NUMBER: 09/764,808
PRIOR PLING DATE: 2001-01-17
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PRIOR PLING DATE: 2001-01-17
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PRIOR PLING DATE: 2001-01-17
PRIOR PLING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,869
PRIOR PLING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,869
PRIOR PLING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US01/01339
PRIOR PLING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US01/01339
PRIOR PLING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US01/01349
PRIOR PLING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US01/01340
PRIOR PLING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US01/01349
PRIOR PLING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US01/01349
PRIOR PLING DATE: 2001-01-17
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PRIOR PLING DATE: 2001-01-17
PRIOR PLING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US01/01349
PRIOR PLING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US01/01349
PRIOR PLING DATE: 2001-01-17
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APPLICATION NUMBER: US01/01239
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APPLICATION NUMBER: 09/764,882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 Sequence 46, Application US/09908711
5 Patent No. US20020045230A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2001-01-17
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Sequence 2543, Application US/09960352
Sequence 2543, Application US/09960352
Patent No. US20020137139A1
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Att, John C.
APPLICANT: Mathialagan, NGSAPPAN C.
APPLICANT: Mathialagan, NGSAPPAN C.
APPLICANT: MATHIALAGAN NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: NUCLEIC ACID AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 2543
LENGTH: 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   997 TCCACCTGGCTGCTGCTGCGGAGGATCCGGGCCGAGTCGGGCACCAAGGGACTCTTTGCA 1056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1057 GGCTTCCTTCCTCGGATCATCAAGGCTGCCCCCTCCTGTGCCATCATGATCAGCACCTAT 1116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            937 CAACGCCAGGTCGCTCTGGGAGCGATGGAGGCTGTGAGAGTGAACCCCCTGCATGTGGAC 996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              511 CAGCGACAAATGTCACTGGGAGCAGTGGAGGCTATGAGAGTGAAGCCGCCAAGAGTTGAC 452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
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OTHER INFORMATION: Genbank Accession No. US20020119462A1 AA926365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.0%; Score 170.2; DB 10; Length 512; 81.7%; Pred. No. 2e-36; tive 0; Mismatches 44; Indels 0;
FILE REFERENCE: 44921-5038-US
FILE REFERENCE: 44921-5038-US
CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31
FRIOR APPLICATION NUMBER: US 60/222,040
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR PLING DATE: 2000-07-31
PRIOR FILING DATE: 2000-011-02
PRIOR FILING DATE: 2001-02-11
PRIOR FILING DATE: 2001-05-11
PRIOR FILING DATE: 2001-05-15
PRIOR PRIOR FILING DATE: 2001-05-15
PRIOR PRIOR FILING DATE: 2001-05-15
PRIOR PLING DATE: 2001-05-25
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LOCATION: (1)..(512)
CTHER INFORMATION: n = a or c or g or t
US-09-917-800A-329
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ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 329
LENGTH: 512
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Best Local Similarity 81.7
Matches 196; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCTGGCCCTGGGCGCCGCCGCACGAGCACCAGCCTAGAGCCAGGACTGAAGCTTCAAG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 ATGGCTGACCAGGACCCTGCGGGCATCAGCCCCTCCAGCAAATGGTGGCCTCAGGCACC 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 ATGGCTGACCAGGACCCTGGGGGCATTAGCCYTC-SCAGCAAATGGTGGCCTCGGGCACT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 GGGGCTGTGGTCACCTCTTTTCATGACGCCCCTGGACGTGGAAGTTCGCCTGCAG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCTCAGCGGCCCTCCATGGCCAGCGAGCTGATGCCTTCCTCCAGACTGTGGAGCCTCTCC 297
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ilarity 82.0%; Pred. No. 5.1e-37;
Conservative 2; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: n equals a,t,g, or c
US-09-908-711-46
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Patent No. US20020119462A1
GENERAL INFORMATION:
APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Castle, Arthur
APPLICANT: Glashoff, Michael
APPLICANT: Gene Logic, Inc.
                               PRIOR APPLICATION NUMBER: USO, 1017
PRIOR PILING DATE: 2001-01-17
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PRIOR PILING DATE: 2001-01-17
PRIOR PILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: USO, 1017
PRIOR PILING DATE: 2001-01-17
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PRIOR PELING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: USO, 10136
PRIOR APPLICATION NUMBER: USO, 01312
PRIOR PILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: USO, 01312
PRIOR PILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: GO/180, 628
PRIOR PILING DATE: 2000-01-31
IOR PELING DATE: 2000-01-31
IOR PELING DATE: 2000-01-31
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PRIOR APPLICATION NUMBER: GO/180, 628
PRIOR APPLICATION NUMBER: GO/209, 467
PRIOR APPLICATION NUMBER: GO/209, 467
PRIOR PELING DATE: 2000-06-07
NUMBER OF SEO ID NOS: 167
LENGTH: 275
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Best Local Similarity
Matches 219; Conserve
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US-09-917-800A-329/c
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LOCATION: (246)
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/ Organism: Dona
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// Organism: Clone ID: 11-LIB34-070-Q1-E1-C11
// Organism: Clone ID: 11-LIB34-070-Q1-E1-C11
// Organism: Clone ID: 11-LIB34-070-Q1-E1-C11
// Best Local Similarity 87.8%; Pred. No. 4.4e-34;
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// Organism: Prof. Conservative 0; Mismatches 25; Indels 1; Gaps 1;
// Organism: Prof. Conservative 0; Mismatches 25; Indels 1; Gaps 1;
// Organism: Orga
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BQ683596 AGENCOURT

ALS.15722 ALS.16722 ALS.16722 ALS.16722 ALS.16722 ALS.16722 ALS.16722 ALS.166 ALS.2036 ALS.2036 ALS.2036 ALS.2036 ALS.2036 ALS.2036 ALS.1846 ALS.1846 ALS.2039 ALS.1846 ALS.2039 ALS.20

Title: Perfect score:

on:

Sequence:

Scoring table:

Searched:

Database

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Functional prediction of the coding sequences of 79 new genes deduced by analysis of cDNA clones from human fetal liver Unpublished
2 (bases 1 to 1402)
Zhang, C., Yu, Y., Zhang, S., Wei, H., Zhang, Y., Zhou, G., Bi, J., Liu, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and Hw.F.
and Hw.F.
Direct Submission
Submitted (13-JAN-1999) Department of Experimental Hematology,
Institute of Radiation Medicine, Beijing Taiping Road 27, Beijing,
Beijing 100850, P. R. China
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1402) Zhang,C., Yu,Y., Zhang,S., Wei,H., Zhang,Y., Zhou,G., Bi,J., Liu,Mand He,F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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BM468665
BQ688847
BM810266
                           AL528266
AL570513
BM915493
BQ949458
BQ934841
AL5194841
AL519919
BM808978
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BG370240
BG4370240
AK002381
BM928609
AL522298
BL333101
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AL563104
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AK007276
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AL571090
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AL545150
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Homo sapiens
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868.4
                            820.4
820.2
818.6
818.8
813.4
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813.4
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805.8
805
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797.2
795.8
790.2
789.4
788.8
788.8
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ACCESSION
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BM923995 AGENCOURT
AL519987 AL519987
AL529906 AL529906
                                                             January 22, 2003, 19:06:17 ; Search time 2432.33 Seconds (without alignments) 10293.906 Million cell updates/sec
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(c) 1993 - 2003 Compugen Ltd.
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AK01939 AMS muscu
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BMS54056
EMS54056.1 GI:18793328
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Contact: Robert Strausberg, Ph.D.
Email: Gapabs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Parayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Biosocience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM12760 row: e column: 06
High quality sequence stop: 691.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/tissue type="meuroblastoma cells"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and Cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Drive Rockwille, Maryland 20850, USA Fax: (1) 301 610 B371 Email: filangelifetech.com URL: http://fulllength.invitrogen.com"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        963 bp mRNA linear EST 13-FEB-2001
Homo sapiens CDNA clone CS0DB005YP09 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 963)
                                                                                                                                                                                                                                                                                                                                 960 GIGGACTCCACCTGNCTGCTGCTGCGGAGGATCGGGGCCGAGTCGGGCACCAGGCAACTC 1019
                                                                                                                                                                                                                                                                                                            GIGGACTCCACCTGCTGCTGCTGCGGAGGATCCGGGCCGAGTCGGGCACCAAGGGACTC 1050
CCCCACTGCCCTTCGAGATGTGCCCTTCTCAGCCCTGTACTGGGTTCAACTATGAGCTGG 780
                                                                                                                                                                                                                             990
                                                             871
                                                                                                      781 TGAAGAGCTGGCTCAATGGGTTCAGGCCGAAAGACCAGACTTCTGTGGGGCATGAGCTTTG 840
                                                                                                                                              931
                                                                                                                                                                                   841 TGGCTGGTGGCATCTCAGGGACGNGGGCTGCAGTGCTGACTCTACCCTTTGACGTGGT-A 899
                                                                                                                                                                                                                                                                 900 AGACCCAACGCCAGGTCCCTCTGGGGAACGATGGAAGCTGTGANAATGAACCCCTGCAT 959
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1. 963
                                                                                                                                              TGGCTGGTGGCATCTCAGGGACGGTGGCTGCAGTGCTGACTCTACCCTTTGACGTGGTAA
                                                                                                                                                                                                                               AGACCCAACGCCAGGTCGCTCT-GGGAGCGATGGAGGCTGTGAGAGTGAACCCCCTGCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Li W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length CDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58.8%; Score 908.8; DB 9; 98.2%; Pred. No. 1.4e-212; iive 3; Mismatches 11;
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/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSODB005YP09"
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                                                                                               /clone_lib="NIH MGC_119"
/tissue_type="medulla"
/lab_host="butlob"
/lab_host="butlob"
/lab_host="butlob"
/note="Organ: brain, Vector: pCNV-SPORT6; Site_l: NotI;
Site_2: ECORV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dr primed and directionally cloned (EcCNV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH MCC Library." 3 others
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Pred. No. 8.9e-213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                            organism="Homo sapiens"
                                                                                   /clone="IMAGE:5742317"
                                                               xref="taxon:9606"
      Location/Qualifiers
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96.2%;
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622 904 8 44 7 44 7 84	80 72 86 86 92 66		110 42 116 36	122 30 128 24	134.	1467
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BM923995 981 bp mRNA linear EST 12-MAR-2002 AGENCOURT\_6709842 NIH\_MGC\_116 Homo sapiens cDNA clone IMAGE:5760154 5', mRNA sequence. BM923995

> LOCUS DEFINITION ACCESSION

RESULT 4 BM923995 BM923995.1 GI:19374374

VERSION

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/db_xref="taxon:Septem="/db_xref="taxon:Septem="/db_xref="taxon:Septem="/db_xref="taxon:Septem="/db_xref="taxon:Septem="/dolo=lib="NiH MoC_li6"
/clone=lib="NiH MoC_li6"
/lab host="DH10B"
/note="Organ: pooled colon, kidney, stomach; Vector:
pCWV-SPORT6; Site 1: Not1; Site 2: ECSNV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male, 49 yo
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EccNV site is
oligo-dT primed and directionally cloned (EccNV site is
destroyed upon cloning). Average insert size 1:4 kb,
insert size range 1-3 kb. Library is normalized and
enziched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4,
                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nh.gov
   Tissue Procurement: Life Technologies, Inc.
   CDNA Library Preparation: Life Technologies, Inc.
   CDNA Library Preparation: Life Technologies, Inc.
   CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
   DNA Sequencing by: Agencourt Bioscience Corporation
   Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
   http://image.llnl.gov
   Plate: LLAM12806 row: 1 column: 11
   High quality sequence stop: 701.
                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 981)

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                                                                                                                                                                 MIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Pred. No. 1.1e-207;
0; Mismatches 23; Indels
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Best Local 8
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SOURCE
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ilarity 97.6%;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1001)
Li,W. B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: Eliang@lifetech.com URL: http://fullength.invitrogen.com" 2 others

9 Length 1001; Indels Score 878.8; DB 9; Pred. No. 3.3e-205; 0; Mismatches 17;

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87 CCACGAGGCGGACGGACGTAATGGGCCCCGCCTGGGCCCCCGCGCCGCCGCACGAGCA

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310 ATGCCTTCCTCCAGACTGTGGAGCCTCTCCTATACCAAATGGAAGTGCCTCCTGTATTGC

AATGGTGTCCTGGAGCCTCTGTACCTGTGCCCAAATGGTGCCCGCTGTGCCACCTGGTTT 387 AATGGTGTCCTGGAGCCTCTGTACCTGTGCCCAAATGGTGCCCGCTGTGCCACCTGGTT 370

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                                                                                                                                                                                                                                                               ALESSORG LTI_NPLOOL_NBC4 HOMO SADIENS CDNA CLONE CSODDOOSYL19 5 Drime, MRNA Sequence.
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/lab_host="DH10B"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
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                             908 GTAAAGA-CCAACGCCAGGTCTGTGGAAG-GATGGGAAGTGTAAGAA-CCCCTG 964
GTAAAGACCCAACGCCAGGTCGCTCTGGGAGCGATGGAGGCTGTGAGAGTGAACCCCCTG 987
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Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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/db xref="taxon:9606"
/clone="CSODD005YL19"
/clone_lib="LTI_NFL001_NBC4"
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Mammalia; Butheria; Primates;
1 (bases 1 to 920)
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Tissue Procurement: DCTD/DTP
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ECORI: CDNA made by oligo-dT priming. Directionally cloned
into ECORI/XhoI sites using the following 5: adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NHT MGC Library."
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                                                                                                                                                                                                                                                                                                                           56.2%; Score 869.4; DB 14; Length 920; 99.7%; Pred. No. 6.5e-203;
                                                                            /db_xxef="taxon:9606"
/clone="MadGs:601198"
/clone=lib="NHH MGC 112"
/tissue_type="melanotic melanoma, cell line"
                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                        /lab host="DH10B (phage-resistant)"
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0; Mismatches 2;
 23
row: m column:
                                                           organism="Homo sapiens"
              High quality sequence stop: 697.
Location/Qualifiers
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 Plate: LLCM2333
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/organism="Homo sapiens"
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 932)

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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2600 row: p column: 15
High quality sequence stop: 616.
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Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LENL)
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Pred. No. 8.2e-203;
0; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
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/note="Organ: brain, Vector: pCMVSPORT 6, 1st strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library is not normalized, but is the control for the normalized libraries. Library was constructed by Life Technologies. Contact: Peng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, maryland 20850, USA Fax: (1) 301 610 8371 Email: http://fulllength.invitrogen.com".
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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/lab_host="DH10B"
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Pred. No. 1.1e-202;
6; Mismatches 13;
                                                                                                                                                                         db_xref="taxon:9606"
/clone="CSODA007YA10"
/clone_lib="LTI_NFL011_NBC1"
/sex="male"
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                     CAGGGTGGCTGGCGCTCACTGTGGCTGGGCTGGGGCCCCCACTGCCCTTCGAGATGTGCCC
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpullished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

DEFINITION

RESULT 9 AL516722 ACCESSION

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Gaps 92 09

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Indels

Length 925;

7 others

152 120 180 272 240 332 300 392 360 452 420 512 480 572 540 632 600 692 099

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ALS70513 LTI_NPL006_PL2 Homo sapiens cDNA linear EST 16-FEB-2001 prime, mRNA sequence.
ALS70513 ALS70513 ALS70513 ALS70513 ALS70513 GI:12926896
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammālia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 910)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
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         66 CGCACGAGCACCAGCCTAGAGCCAGGACTGAAGCTTCAAGATGGCTGACCAGGACCCTGC 125
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                                               GGGCATCAGCCCCCCCAGCAAATGGTGGCCCTCAGGCACCGGGGCTGTGGTTACCTCTCT
                                                                           126 GGGCATCAGCCCCCTCCAGCAAAAGGGGCCTCAGGMACCGGGGCTGTGGTTACCTCTCT
                                                                                                                    CTTCATGACACCCCTGGACGTGGAGGTTCGCCTGCAGTCTCAGCGGCCCTCCATGGC
                                                                                                                                       CAGCGAGCTGATGCCTTCCTCCAGACTGTGGAGCCTCTCCTATACCAAATGGAAGTGCCT
                                                                                                                                                                                                                          246 CAGCGAGCTGATGCCTTCCTCCAGACTGTGGAGCCTCTCCTATACCAAATGGAAGTGCCT
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1 (bases I to 911)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length CDM libraries and normalization
Unpublished (2001)
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                                                                                              721 -CCCACTGCCCTTCGAGATGTGCCCYTCTCAGCCCTGTACTGGTTCAACTATGAGCTGGT 779
                                                                                                                                                    871
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                      TCCCTGTGTTCGAACTGCAGTGGCTCAGGGTGGCTGGCGCTCACTGTGGCTGGGCTGGGG
                                                                                                                                           813 GAAGAGCTGGCTCAATGGGTTCA-GGCCGAAGGACCAGACTTCTGTGGGGCATGAGCTTTG
                                                                       CCCCACTGCCCTTCGAGATGTGCCCTTCTCAGCCCTGTACTGGTTCAACTATGAGCTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
_Location/Qualifiers
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Best Local Similarity 96.7
Matches 876; Conservative
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                                                                        Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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  Full-length cDNA libraries and normalization Unpublished (2001)
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Matches 868; Conservative
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 959)
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TCTCTCCCACGGATGGGGAGAGGCCAGGAGGAGCCCAGCCAAGTGCCTTTTCCTCAGCA 1258
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCX2006 row: column: 08
High quality Sequence stop: 687.
Location/Qualifiers
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/organism="Homo sapiens"
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Tissue Procurement: DCTD/DTP
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Best Local Similarity 96.73
Matches 916; Conservative
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/note="Cryan: lung; Vector: pOTB7; Site 1: Xho1; Site 2:
EcoR1; cDNA made by oligo-dT priming. Directionally cloned
into EcoR1/Xho1 sites using the following 5: adaptor:
GGGACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
BerKeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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larity 96.7%; Pred. No. 4e-199;
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 939 bp
 mRNA
 linear
 EST 21-AUG-2002

 AGENCOURT 8824335 NIH\_MGC\_18 Homo sapiens cDNA clone IMAGE:6459569
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 BQ949458
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 GI:22364936

BQ949458 LOCUS DEFINITION

RESULT 13

ACCESSION VERSION KEYWORDS SOURCE

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/clone="INAGE:642317"
/clone=lib="NTH MGC 18"
/tissue_type="large cell carcinoma"
/lab_nost="Emblo Repage-resistant"
/note="Organ: lung; Vector: poTB7; Site 1: XhoI; Site 2:
BcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRIX/XhoI sites using the following 3: adaptor:
GGCACCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
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AGENCOURT_8824927 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:6423317
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
11 (bases 1 to 965)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can k
found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLCM2601 row: 1 column: 06
High quality sequence stop: 626.
   CGCCACCCTGGTGATGACTGTGCCAGCTACCGCCATCTACTTCACTGCCTATGACCAACT
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
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Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NHH MGC Library." a 308 c 295 g 197 t 4 others
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

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Location/Qualifiers
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January 22, 2003, 19:04:17; Search time 3022.46 Seconds (without alignments) 10726.543 Million cell updates/sec 1 ctgaagcttcaagatggctg.....aggggcaaggaggcaaggac 1114 4109280 number of hits satisfying chosen parameters: 2054640 seqs, 14551402878 residues Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries OM nucleic - nucleic search, using sw model Gapop 10.0 , Gapext 1.0 em\_htgo\_hum:\* em\_htgo\_mus:\* em\_htgo\_other:\* em htg hum: \*
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RESULT 1
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DEFINITION Sequence 1 from Patent W00198355.
AX403084 I GI:21388033
VERSION Ax403084.1 GI:21388033
SOURCE human.
ORGANISM Homo sapiens
ELKETYOTE NETAZOA; Chordata; Craniata; Vertebrata; Euteleostomi;
MAMMMAIA; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE Lewin, D., Adams, S.H. and Yu, X.X.
TITLE Cgi-69 compositions and methods of use
JOURNAL Patent: WO 0198355-A 1 27-DEC-2001;

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100.0%; Score 1114; DB 6;
100.0%; Pred. No. 5.4e-244;
ive 0; Mismatches 0;
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                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
_349 c 332 g 239
                        Genentech, Inc. (US)
                                                                                                                                              Conservative
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Best Local Simil
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DVVKTOROVALGANEAAVRAVPLHVDSTWILLERRIRAESGTKGLFAGFLPRIIKAAPSC
AIMISTYFFGKSFFQRLNQDRILGG"
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/product=-micochondrial carrier protein CGI-69 long form"
/protein id="Add60687.1"
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1 (bases 1 to 1114)

Yu.X. Lewin, D.A., Zhong, A., Brush, J., Schow, P.W., Sherwood, S.W., Pan, G. and Adams, S.H.

Overexpression of the human 2-oxoglutarate carrier lowers mitochondrial membrane potential in HEK-293 cells: Contrast with the unique cold-induced mitochondrial arrier CGI-69

Biochem. J. 353 (Pt 2), 369-375 (2001)
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Yu, X.X., Lewin, D.A., Zhong, A., Brush, J., Schow, P.W., Sherwood, S.W., Pan, G. and Adams, S.H.
Dracet Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens mitochondrial carrier protein CGI-69 long form mRNA, complete cds.
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/db_xref="taxon:9606"
/tissue_type="liver"
14. .1093
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Best Local Similarity 100.0%;
Matches 1114; Conservative 0;
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HSM801436	Homo sapiens mR complete cds. AL133584 AL133584.1 GI:	human. Homo sapiens Eukaryota; Meta	Mammalia; Buthe 1 (bases 1 to Wiemann,S., Wei Ansorce,W., Boe	Lauber,J., Dues Mewes,H.W., Ott Wambutt,R., Kor Toward a Catalo	Analysis of 500 Genome Res. 11 11230166 2 (bases 1 to	Poustka, A., Kle Direct Submissi Submitted (15-D Martinsried, GE	Clone from S. W Research Center sequenced by DK Heidelberg/Germ	German Genome P This clone (DKF Please contact Berlin-Charlott	information abo at http://www.m Locati 1. ,15	/organ /db_xr /chrom /clone	/tissu /clone DH10B; /dev_s	118 /gene= /gene= . /gene= /gene=	/note= carrie /codon /produ	/prote /db_xr /db_xr /trans	SMASEL FVKIVR ALARLG VPFSAL	VALGAM FGKSFF ite 1540 278 a 49	UGIN  Query Match  Best Local Similarity 9
RESULT 3 HSM801436 LOCUS	DEFINITION ACCESSION VERSION		REFERENCE AUTHORS	TITLE	JOURNAL PUBMED REFERENCE		COMMENT		FEATURES			gene				polyA_sit	ORIGIN Query Matc Best Local
61 GGCCTCAGGACCGGGGCTGTGGTTACCTCTCTTCATGACACCCCTGGACGTGGTGAA 120	121 GGTTCGCCTGCAGTCTCAGCGGCCCTCCATGGCCAGCGAGGCTTCCTCCAGACTCATGCCTTCCTCAGACTCATGCCTTCCTCCAGACTCATGGCTTCCTCAGAGCTCATGGCCTCCATGGCCAGCGAGCG	181	241 GTATTGCAATGGTGTCCTGGAGCCTCTGTACCTGTGCCCAAATGGTGCCCGCTGTGCCAC 300	301 CTGGTTTCAAGACCCTACCCGCTTCACTGGCACCATGGATGCCTTCGTGAAGATCGTGAG 360 	361 GCACGAGGGCACCAGGACCCTCTGGAGGGGCCTCCCGGCACCCTGGTGATGACTGTGCC 420	421 AGCTACCGCCATCTACATGCCTATGACGACTGAAGGCCTTCCTGTGGGTCGAGC 480	481 CCTGACCTC1 ACCTCTACGCACCCCATGGTGGCTGGCGCTGGCCCGCCTGGGCCCGC 540	541 GACTGTGATCAGCCCCTGGAGCTTATGCGGACAAAGCTGCAGGCTCAGCATGTGTGTG	601 CCGGGAGCTGGGTGCTGTGTTCGAACTGCAGTGGGCTGGGCTGGCT	661 GCTGGGCTGGGGCCCCACTGCCCTTCGAGATGTGCCCTTCTCAGCCCTGTACTGGTTCAA 720	721	781 CATGAGCTTTGTGGCTGGTGGCATCTCAGGACGGTGGCTGCAGTGGTGACTCTACCCTT 840	841 TGACGTGGTAAAGACCCAACGCCAGGTCGCTCTGGGAGCGATGGAGGCTGTGAGAGTGAA 900 		961 CAAGGGACTCTTTGCAGGCTTCCTTCCTCGGATCATCAAGGCTGCCCCTCCTGTGCCAT 1020	1021 CATGATCAGCACCTATGAGTTCGGCAAAAGCTTCTTCCAGAGGCTGAACCAGGACCGGCT 1080	1081 TCTGGGCGCTGAAAGGGCAAGGAGCAAGGAC 1114 
\( \frac{1}{2} \)	SS qq	Oy Dp	9y 0b	Qy Db	G qq	Qy Dp	\$ 65 60	QV Dp	\$ 90 90	Qy Db	QQ QQ	qa )	\$ a	Qy aa	QV QD	Q7 Db	\$\$ qa

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Project.

KFZp434C119) is available at the RZPD in Berlin.

t the RZPD: Ressourcententrum, Heubnerweg 6, 14059

tenburg, GERMANY; Email: clone@rzpd.de Further

bout the clone and the sequencing project is available.

mips.blochem.mpg.de/proj/cDNA/.
1550 bp mRNA linear PRI 10-MAR-2001 nRNA; cDNA DKFZp434C119 (from clone DKFZp434C119);
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%LMPSSRLMSLSYTKWKCLLYCNGVLEPLYLCPNGARCATWFQDPTRFTGTMDA
RHEGTRTLMSGLPATLVMTVPATAIYFTAYDQLKAFLCGRALTSDLYAPMVAG
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LYWFNYELVKSWINGLRPKDQTSVGMSFVAGGISGTVAAVLTLPFDVVKTQRQ
MEAVRVNPLHVDSTWLLLRRIRAESGTKGLFAGFLPRIIKAAPSCAIMISTYE
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s="CG1-69 protein, strong similarity to mitochondrial
er proteins"
                                                                                                                                                                                                                                                                                                                                               eil, B., wellenreuther, R., Gassenhuber, J., Glassl, S., Oscher, M., Bloecker, H., Bautersachs, S., Blum, H., estrachoeft, A., Beyer, A., Kochrer, K., Strack, N., tenwaclder, B., Obermater, B., Tampe, J., Heubner, D., Orn, B., Klein, M. and Poustka, A.

Orn, B., Klein, M. and Poustka, A.

Olog of Human Genes and Proteins: Sequencing and 00 Novel Complete Protein Coding Human CDNAs

1 (3), 422-435 (2001)
                                                                                                                                                                                                                                                       azoa; Chordata; Craniata; Vertebrata; Eutelecstomi;
Heria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wiemann, Molecular Genome Analysis, German Cancer ar (DKRZ); Beali s. wiemannsökfz- Heidelbeig.de; DKRZ (German Cancer Research Center, German Cancer Research Center, and within the CDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ne="DKFZp434Cl19"
Nue type="Lestis"
Lib="434 (synonym: htes3). Vector pSporti; host
3; sites NotI + SalI"
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ein_id="CAB63728.1"
rref="GI:6599170"
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kref="taxon:9606"
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ALARLGTYTUSPLELMRTLQAQLWYSYELGACVRTAVAQGGWESLWLGWGPTALRD
VPRSALYWFNYELWGSWLNGLFPKDQTSVQASFYAGGI SGTVAAVITLEPDVWKTQRQ
VARGALWWFNYELWSWLLLKRRTRAESGTKGLPAGFLFRI IKAAFSCAIMISTYE
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Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Zhang,L.-H. and Green,E.D.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 26 Row: g Column: 12.
                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (12-JUN-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                    complete cds
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/protein_id="AAH09330.1"
/db_xref="GI:14424606"
                                                                                                                                               Homo sapiens, clone MGC:16684 IMAGE:4126268, mRNA, BC009330
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/clone lib="NIH MGC 19"
/lab host="DH10E-R"
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97.8%; Pred. No. 9.3e-231;
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/clone="MGC:16684 IMAGE:4126268"
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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CTGAAGCTTCAAGATGGCTGACCAGGACCCTGCGGGCATCAGCCCCCCTCCAGCAAATGGT 60

Db 1146 TCTGGGCGGCTGAAAGGGGCAAGGAC 1179	AX403085	EFINITION Sequence 2 from Patent CCESSION AX403085 ERRION AX403085.1 GI:2138803 EYWORDS	OURCE ORGANISM	REFERENCE Lewin, D., Adams, S.H. and Yu, X.X.  TITLE Cg1-69 compositions and methods of use JOURNAL Patent: WO 0198355-A 2 27-DEC-2001;	Genentech, Inc. (US); Curagen Corporation (US)  Location/Qualifiers  Location/Qualifiers  source  Corporation (US)  Location/Qualifiers  Location/Qualifiers  Asherical (US)	BASE COUNT 272 a 489 c 459 g 326 t  ORIGIN	Query Match 94.6%; Score 1054.4; DB 6; Length 1546; Best Local Similarity 97.8%; Pred. No. 2.2e-230; Matches 1089; Conservative 0; Mismatches 1; Indels 24; Gaps 1;	Oy 1 CTGAAGCTTCAAGATGGCTGACCAGGACCCTGCGGGCATCAGCCCTCCCAGCAAATGGT 60	Oy 61 GCCTCAGGCACCGGGCTGTGGTTACCTCTCTTCATGACACCCTGGACGTGGAA 120	Qy 121 GGTTCGCCTGCAGTCTCAGCGGCCTCCATGGCCAGCGAGCTGATGCCTTCCTCCCAGCT 180	Qy 181 GTGGAGCCTCTCCTATACCAAATTGCCCTCCTCTCCAATCCACAGGGAAGTGCCTCCT 240	Qy 241 GTATTGCAATGGTGTCCTGGAGCCTCTGTACCTGTGCCCAAATGGTGCCCGCTGTGCCCA 300  1	Qy 301 CTGGTTTCAAGACCCTACCGGTTCACTGGCACCATGGATGCCTTCGTGAAGATCGTGAG 360	Qy         361         GCACGAGGGCACCAGGACCTCTGGAGGGCCTCCCCCCCCC	A21 AGCTACCGCCATCTACTGCCTATGACCAACTGAAGGCCTTCCTGTGTGGTGGAGC 480	QY         481         CCTGACCTCTACGCACCCATGGTGGCTGGCCGCTCGGCCCGCTGGGCACCGT         540           DS         561         CCTGACCTCTGACCTCTACGCACCCATGGTGGCTGGCCGCGCTGGCCTGGGCACCGT         620	by 541 GACTGTGATCAGCCCCTGGAGCTTATGCGGACAAAGCTGCAGGATGTGTCGTA 600	Oy 601 CCGGGAGCTGGGTGCCTGTGTTCGAACTGCAGTGGCTGGC
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/bc.xeef="G14929607" |
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1. 1556
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1. (Dases 1 to 1556)
Lai, C.H., Chou, C.Y., Ch'ang, L.Y., Liu, C.S. and Lin, W.
Identification of novel human genes evolutionarily conserved in Caenorhabdits elegans by comparative proteomics

Genome Res. 10 (5), 703-713 (2000)
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/product="CGI-69 protein"
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/db_xref="taxon:9606"
/chromosome="17"
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                                                                                                                                                                                                                                                   bcu01398 15-79 bp mRNA linear PRI 12-JUL-2001
Homo sapiens, CGI-69 protein, clone MGC:1163 IMAGE:3051436, mRNA,
complete cds.
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"Netherbo, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,
Shevcherko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,
Benjamin, B., Blakesley, R.W., Boulfard, G.G., Brinkley, C., Brooks, S.,
Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,
Lim, M., Maduro, Q.L., Masiello, C., Mastrian, S.D., Mccloskey, J.C.,
McDowell, J., Pearson, R., Snyder, B., Stantripop, S., Thomas, P.J.,
Thongson, E.E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A.,
Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="madodPag1SPLOQMVASGTGAVVTSLFMTPLDVVKVRLQSGRP
SMASELMPSSRLWSLSYTKWKCLLYCNGVLEPLYLCPNGARCATWFQDPTRFTGTMDA
FVKIVRHEGTRTLWSGLPATLVMTVPATAIYFTAYDQLKAFLCGRALTSDLYAPMVAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: http://image.llnl.gov Series: IRAL Plate: 4 Row: o Column: 13
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 10438782.
                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 1579)

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (12-DEC-2000) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
CAAGGGACTCTTTGCAGGCTTCCTTCCTCGGATCATCAAGGCTGCCCCCTCTGTGCCAT 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The 1.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                 1101 CATCATCAGCACCTATGAGTTCGGCAAAAGCTTCTTCCAGAGGCTGAACCAGGACCGGCT
                                                       CATGATCAGCACCTATGAGTTCGGCAAAAGCTTCTTCCAGAGGCTGAACCAGGACCGGCT
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/organism="Homo sapiens"

/db_xref="LocusID:51629"

/db_xxef="taxon:9606"

/clone="MGC:1163 IMAGE:3051436"

/tissue_type="folion, adenocarcinoma"

/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC Project URL: http://mgc.nci.nih.gov
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                                                                                                                               TCTGGGCGGCTGAAAGGGGCAAGGACCAAGGAC 1114
                                                                                                                                                             TCTGGGCGGCTGAAGGGCCAAGGAGGCAAGGAC 1194
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/product="CGI-69 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAH01398.1"
/db_xref="GI:12655093"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                             BC001398.1 GI:12655092
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Web site: http://
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Homo sapiens
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JOURNAL
                   1041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
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KF RDS
                                                                                                                                                                                                                                               BC001398
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VPFSALYWFNYELVKSWLNGFRPKDQTSVGMSFVAGGISGTVAAVLTLPFDVVKTQRQ
VALGAMEAVRVNPLHVDSTWLLLRRIRAESGTKGLFAGFLPRIIKAAPSCAIMISTYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178 GGCCTCAGGCACCGGGCTGTGGTTACCTCTCTTCATGACACCCCTGGACGTGGTGAA 237
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                                                                                                                                                                                         Length 1579;
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                                                                                                                                                                                         DB 9;
                                                                                                                                                                                      94.6%; Score 1054.4; DB 9 97.8%; Pred. No. 2.2e-230;
                                                                                                                                                                                                                                                 0; Mismatches
                                                                                              326
                                                                                           464 g
                                                             FGKSFFQRLNQDRLLGG"
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Db 648 CCTGACCTCTG Oy 541 GACTGTGATCA Db 708 GACTGTGATCA Oy 601 CCGGG.CCTGG Oy 661 GCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG			RESULT 9 AKO2660 DECUS DEFINITION Home sapi ACCESSION AKO26060 KEYWORDS SOURCE SOURCE Home sapi CORGANISM Home sapi CORGANISM Home sapi AMMANISM AMMANISM AMMANISM AMMANISM AMMANISM AND SAPI AMMANISM AND SAPI AMMANISM AND SAPI AMMANISM AND SAPI AND HOME SOURNAL UNDUBLIST AUTHORS SUGANERS SUGANERS AUTHORS SUGANERS SUGANERS AUTHORS SUGANERS SUGANERS AUTHORS SUGANERS SUGANERS AUTHORS SUGANER	TITLE Direct Standard Countree Comment NEDO human CE Comment NEDO human International Country
Db   994   CCCCTGCATGTGAACTCCACCTGGCTGCTGCGGAGTCCGGGCCGAGTCGGGCAC 1053	### ARILEGIS   PARTIEGIS   1643 bp   DNA   linear PAT 16-MAY-2001   DEFINI TON Sequence 68 from patent US 6132973.   ARILEGIS   ARIL	Query Match         94.6%; Score 1054.4; DB 6; Length 1643;           Best Local Similarity 97.6%; Pred. No. 2.1e-230;           Matches 1089; Conservative 0; Mismatches 1; Indels 24; Gaps 1;           Qy           192 CTGAAGCTTCAAGATGGCTGACCAGGACCTGGGGCATCAGCCCCTCCAGCAAATGGT 60           Db           192 CTGAAGCTTCAAGATGGCCTGACCAGGACCTGGGGGATCAGCCCCTCCAGCAAATGGT 251	61 252 121 121 312 372 468 468 468 468	GCACGAGGCACCATCACTACTACTACTACTACTACCCCGCCACCCTGGTGATGACTGTGCC  AGCTACCGCCATCTACTTCACTGCCTATGACCACCTGCCTG

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ies I to 1554)

S. Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Isogai, T.,

ra, T., Tanaka, T. and Nakamura, Y.

Submission

sed (29-MG-2000) Sumio Sugano, Institute of Medical Science,

sity of Tokyo, Laboratory of Genome Structure Analysis, Human
Center, Shirokame-dai, 4-6-1, Minato-ku, Tokyo 106-8639,

E-mail:cdnai@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRI 29-SEP-2000
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a, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T.,
a,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
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piens primary human renal epithelial cells cDNA to mRNA,
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Zhang C., Yu Y., Zhang S., Wei H., Zhang Y., Zhou G., Bi J., Liu M., He F. "Functional prediction of the coding sequences of 79 new genes deduced by analysis of CDNA clones from human fetal liver"; Unpublished.
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Department of Experimental Hematology, Institute of Radiation Medicine,
Beijing Taiping Road 27, Beijing, Beijing 100850, P. R. China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATGATCAGCACCTATGAGTTCGGCAAAAGCTTCTTCCAGAGGCTGAACCAGGACCGGCT 1080
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Eutheria, Primates, Catarrhini, Hominidae, Homo.
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(Rel. 67, Last upd
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VALGAMBNVRVNHTHVDSTWLLLRRIRAESGTKGLFAGFLPRI IKAAFSCAIMI STYE
FGKSFFQRLNQDRLLGG"
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SMASELMPSSRLWSLSYTKWKCLLYCNGVLEPLYLCPNGARCATWFQDPTRFTGTMDA
FVKIVRHEGTRTLWSGLPATLVMTVFATAIYFTAYDQLKAFLCGRALTSDLYAPMVAG
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sequencing: Research Association for Biotechnology, cDNA library construction, 5'- & 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology
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                                                                                                                                                                                                                                                                          /protein_id="BAB15341.1"
/db_xref="G1:10438783"
                                                                                                                    /organism="Homo sapiens"
/db xref="taxon:9606"
/clone="HRC08407"
                                                                                     Location/Qualifiers
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AUTHORS
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                                                                                                                                                                                 /protein_id="AAF69618.1"
/translation="MYASGTGAVVTSLFMTPLDVVKVRLQSQRPSMASELMPSSRLWSL
SYTKWKCLLYCNGVLEPLYLCPNGRCATWFQDPTRFTGTMDAFVKTVRHEGTRTLWSC
LPATIVMYTVPATATYFTAYDQLKAFLGRALITSDLYAPMVAGALARLGTVTVTSPLEIM
                                                                                                                                                                                                                                               RTKLQAQHVSYRELGACVRTAVAQGGWRSLWLGWGPTALRDVPFSALYWFNYELVKSWL
                                                                                                                                                                                                                                                                  NGLRPKDQTSVGMSFVAGGISRTVAAVLTLPFDVVKTQRQVALGAMEAVRVNPLHVDST
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                                                                                                                                                                                                                                                                               WLLLRRIRAESGTKGLFAGFLPRIIKAAPSCAIMISTYEFGKSFFQRLNQDRLLGG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                233 TGCCTCCTGTATTGCAATGGTGTCCTGGAGCCTCTGTACCTGTGCCCAAATGGTGCCCGC 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           217 TGTGCCACCTGGTTTCAAGACCCTACCGGCTTCACTGGCACCATGGATGCCTTCGTGAAG 276
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                                                                                                                                                                                                                                                                                                                                                                                                        53 CAAATGGTGGCCTCAGGCACCGGGGCTGTGGTTACCTCTCTTCATGACACCCCTGGAC 112
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                                                                                                                                                                                                                                                                                                              Sequence 1402 BP; 261 A; 432 C; 401 G; 308 T; 0 other;
                                                                                                                                           /note="predicted protein of HQ2163"
/product="PRO2163"
                                                                                                                       /codon_start=1
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                                            'organism="Homo sapiens"
                                                      /clone="FLB8041"
/tissue_type="liver"
/dev_stage="fetus"
4. .1017
                           _xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                             90.08;
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Matches 1037; Conservative
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HTG 06-NOV-2001
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 173434)
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Direct Submission
Unpublished
Upublished
(Loses 1 to 173434)
Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.
Direct Submission
Submitted (OsNOV-201) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA
On Nov 6, 2001 this sequence version replaced gi:13157584.
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TCTGTGGGCATGAGCTTTGTGGCTGGTGGCATCTCAGGGACGGTGGCTGCAGTGCTGACT
                                            CTACCCTTTGACGTGGTAAAGACCCAACGCCAGGTCGCTCTGGGAGCGATGGAGGCTGTG
                                                                                                                                                                                            757 chaccerrigaceregrapasacceaaceceaegreecreregeaecearecaegrere
                                                                                                                                                                                                                                                             893 AGAGTGAACCCCCTGCATGTGGACTCCACCTGGCTGCTGCGGAGGATCCGGGCCGAG
                                                                                                                                                                                                                                                                                                         817 AGAGTGAACCCCTGCATGTGGACTCCACCTGGCTGCTGCGGAGGATCCGGGCCGAG
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HTG; HTGS_PHASE1; HTGS_BRAFT; HTGS_FULLTOP; HTGS_ACTIVEFIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC098934 1173434 bp DNA linear HTG 06
Homo sapiens chromosome 1 clone RP11-480112, WORKING DRAFT
SEQUENCE, 6 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insert size: 172934; sum-of-contigs
Quality coverage: 8.7x in Q20 bases; sum-of-contigs
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Sequencing vector: plasmid; LO8752; 68% of reads
Chemistry: Dye-terminator ET; 89% of reads
Chemistry: Dye-terminator Big Dye; 11% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: University of Washington Genome Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1073 GACCGCCTTCTGGGCGGCTGAAGGGGCAAGGAGCAAGGAC 1114
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Center clone name: RP11-480112 (sc0719)
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765

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E Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banke,T., Babbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banke,T., Barbaria,J., Benton,J., Binage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Bunky,C., Burch,P., Burkerl,C., Burchl,R., Oracco, Cackon,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Dragoc,O., Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earnautt,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Radwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Falls,T., Forcia,M., Garnex,T., Garza,N., Gill,R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA linear HTG 13-JUL-2002
*** SEQUENCING IN PROGRESS ***,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                               16051 ---CTGAGCCCTTACCTCTACATAACCTTGGTAGCTGGTGGTGGTGGTCCACCCTGGCACT 16107
                                                                                                                                            16108 ATCACTGCAATCATCAGTGCCCTGGAGCTTATGCAGACAAAGCTGCAGGTTTAGCATATG 16167
                                                                                                                                                                                                                                                                                                                               16347 CCCATGACAACCATAGGAGTCAGCTTTGCAGCTGGCAGCATCACCATGATGCTGGCTACA 16406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16586 ATCCCCTCCTATGCTATCACGATCACCACTTATGAGTTCAGCAAAAGTCTCTTAAAGAA 16645
                                                                                                                                                                                                                                                   16168 TIMIACIMIGEGET-GGIACCIGIGITITGAGCICCGGIGGCTIAGAGIGGIIGGIGCICA 16226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1004 GCCCCCTCCTGTGCCATCATGATCAGCACCTATGAGTTCGGCAAAAGCTTCTTCCAGAGG 1063
                      16287 ITCAACTACGAGCTAGTGAAGAGCTGGCTGAATGGGCTCAGGCCAAAGGAACTCCATGGT
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twis or N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                         contig of 9114 bp in length
gap of unknown length
contig of 17991 bp in length
app of unknown length
contig of 20346 bp in length
gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 651; DB 2; Length 17:
Pred. No. 1.9e-138;
0; Mismatches 190; Indels
                                                                                                                                                                                                                                                                                            2 112038: contig of 37817 bp in length
9 112138: gap of uknown length
9 17434: contig of 61296 bp in length.
Location/Qualifiers
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Gorrell J.H. Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgason, A., Hogues, M., Holloway, C., Hollins, B., Henmai, F., Howard, S., Huber, J., Holloway, C., Hollins, B., Jacobson, B., Jia, Y., Johnson, R., Jollyet, S., Joudah, S., Kari, V., Kan, U., Karden, J., Kovar, C., Karshi, A., Landry, M., Leal, B., Lewis, L., Lewis, L., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Li, J., Lu, X., Lucier, A., Lucier, R., Lun, R., Martinez, E., Massey, E., Mawhiney, E., Martin, R., Martinale, A., Martinez, E., Massey, E., Mawhiney, E., Martin, R., Martinale, A., Martinez, E., Minner, G., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Minner, C., Mitchell, T., Mohabbat, R., Mornis, S., Nguyen, N., Nogyen, N., Nogyen, N., Nogyen, N., Nogyen, N., Nogyen, M., Nogyen, M., Nogyen, R., Pace, A., Payton, B., Peery, J., Perer, J., Perer, J., Rives, M., Rojas, A., Rojubokan, I., Shooffari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sucokens, R., Patinus, E., Pull, L., Quilles, M., Ruis, S., Satton, Schen, H., Shooshari, N., Sisson, I., Sodergren, E., Sonaike, T., Patks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Talfrod, B., Thomas, M., Tamerisa, A., Tamerisa, K., Wand, Moore, S., Warren, R., Washington, C., Watlington, S., Wallshams, G., Willalams, A., Walle, M., Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Virson, D., Virson, D., Virson, D., Virson, D., Virson, D., Virson, D., Virson, D., Virson, D., Virson, D., Virson, D., Virson, D., Virson, D., Virson, D., Virson, D., Virson, D., Virson, D., Virson, D., Virson, D., Virson, D., Virson, D., Virson, D., Virson, D., Virson, D., Virson, D., Virson, D., Virson, D., Virson, D., Virson, D., Virson, D., Virson, D., Virson, D., Virson, D., Virson, D., Virson, D., Virson, D., Virson, D., Virson, D., Virson, D., Virson, D., Virson, D., Virson, D., Virson, D., Virson, D., Virson, D., Virson, D., Virson, D., V
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NOTE: This is a 'working draft' sequence. It currently consists of 29 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 3, 2002 this sequence version replaced gi:21239891.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (29-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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1534: gap of unknown length
3218: contig of 1684 bp in length
3318: gap of unknown length
4531: contig of 1213 bp in length
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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                                                                     77889 GATTCTGGAGTCTTTCCTACACCAAATCACCCTCCTCTTACAATCCCCCAGTGACATGCT
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ACT19489-3
ACT19489-3
Continuation (4 of 4) of ACT19489
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Wartun, D.M. Adama, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Albarocks, S. L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Balbarocks, S. L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Balbarocks, S. L., Amaratunge, H.C., Branch, M., Banks, T., Balbarocks, S. L., Amaratunge, H.C., Burrell, K.L., Byrd, M.C., Chen, G., Chen, R., Cavazos, S.R. Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, C., Coyle, M.D., Dathorne, S.R., David, R., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davis, C., Elajo, M., Ederzich, D., And, R., Davis, C., Elajo, M., Ederzich, D., Ranter, C., Edgar, D., Edwards, C.C., Elhajo, T., Eoster, P., Frantz, P., Barris, C., Harris, K., Harr, M., Havlak, P., Hawes, A., Harnandez, J., Garcia, A., Garrier, T., Garzia, N., Gill, R., Gorsis, R., Garcia, A., Garrier, P., Hane, J., Halber, S., Hamilton, K., Harris, C., Harris, K., Harr, M., Havlak, P., Hawes, A., Harniton, E., Honsis, R., Johnson, R., Joliver, S., Joudah, S., Joudah, S., Jacobson, B., Jia, Y., Johnson, R., Joliver, S., Joudah, S., Martinez, B., Martin, R., Mayus, C., Hun, J., Kureshi, A., Landry, N., Leal, B., Leady, J., Martin, R., Mayus, M., Marton, J., Kureshi, A., Landry, N., Leal, B., Martin, R., Mayus, M., Micherson, E., Martin, R., Mayus, R., Martin, R., Mayus, M., Micherson, E., Martin, R., Mayus, R., Marton, C., Minner, Z., Mutchell, T., Mohabbat, K., Moyen, M., Noriedo, M., Polibokan, I., Rolfe, M., Rolfe, M., Rute, S., Soulke, T., Sparks, A., Tameris, A., Tameris, A., Tameris, A., Tameris, J., Tomas, M., Rute, S., Soulke, T., Yerk, A., Palbron, D., Villalon, D., Villalon, D., Villalon, D., Villalon, D., Wall, M., Wut, Y., Wut, Y., Wut, Y., Wut, Y., Wut, Y., Wut, Y., Wut, Y., Wut, Y., Wut, Y., Wu
156175 bp DNA linear HTG 13-JUL-2002
Rattus norvegicus clone CH230-161G12, *** SEQUENCING IN PROGRESS
***, 66 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
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* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 66 contigs. The true order of the pieces

* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of M, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                Sequencing vector: Plasmid,
Sequencing vector: Plasmid,
Assembly program: Phrap; version 0.990329
Consensus quality: 99973 bases at least Q40
Consensus quality: 106615 bases at least Q40
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Rattus norvegicus clone CH230-75J9, *** SEQUENCING IN PROGRESS ***, A0124203
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
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                                    CTTCGTGAAGATCGTGAGGCACGAGGCACCAGGACCCTCTGGAGCGGCCTCCCCGCCAC 402
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NOTE: This is a 'working draft' sequence. It currently consists of 60 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (13-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 195701)
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Submitted (24-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
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On Jun 17, 2002 this sequence version replaced gi:21397217.
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Center clone name: CH30-75J9
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Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 149658 bases at least Q40
Consensus quality: 149658 bases at least Q30
Consensus quality: 153360 bases at least Q20
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Contact: hgsc-help@bcm.tmc.edu
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This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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	36	74.8	6.7	496	22	AAK07540	Human brain expres
	37	74.8	6.7	496	22	AAK33336	Human bone marrow
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PI Lewin D, Adams SH, Yu XX;

XX WPI; 2002-114569/15.

XX CGI-69 polypeptides and polynucleotides useful for treating metabolic disorders including cachexia, obesity, diabetes and cancers disorders including cachexia, obesity, diabetes and cancers.

XX Claim 1(a); Page 9-10; 107pp; English.

XX Claim 1(a); Page 9-10; 107pp; English.

XX Claim 1(a); Page 9-10; 107pp; English.

XX CAMSOS69), a novel splice variant of human CGI-69. Various CGI-69 concluders included from human liver upon PCR amplification and clones were isolated from human liver upon PCR amplification and clones were isolated from human liver upon PCR amplification and clones were isolated from human liver upon PCR amplification and clones were isolated from human liver upon PCR amplification and clones diversed from the previously known CGI-69 concluders in relates to a novel characterization of CGI-69. CC The invention relates to a novel characterization of CGI-69 as a mitochondrial carrier protein, the discovery of CGI-69. CGI-69 concluding overspression of carboxyl-EnAG-14gged CGI-69. And PLO CC chrouply oversexpression of carboxyl-EnAG-14gged CGI-69. CGI-69 cGI-69. CGI-69 cGI-69. CGI-69 cGI-69. CGI-69. CGI-69. CGI-69. CGI-69 concluding and treating metabolic diseases in humans, including cplicate tissue (BAT) is presented. The mouse orthologe a cissue (BAT) is presented. The mouse orthologe a cissue (BAT) is presented. The mouse orthologe a cissue (BAT) is presented. The mouse orthologe a cissue of increasing or decreasing mitochondrial membrane potential in brown cc contexts of increasing or decreasing docy weight. Decreasing the activity of CGI-69 through gene therapy provides a means of treating metabolic diseases, such as obesity or cachexia, colimical collections and bacterial infections and bacterial infections (CGI-69 through gene therapy provides a mutation in the CGI-69 gene.

CC dampered by 194 A, 349 C, 332 G, 239 T, 0 other;
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SQ Sequence 1114 BP; 194 A; 349 C; 332 G; 239 T; 0 other;
Ouery Match

Best Local Similarity 100.0%; Pred. No. 4.3e-264;
Matches 1114; Conservative 0; Mismatches 0; Indels 0; Gaps
ON 1 CHICARACHTGRACHGRACHGRACHGRACHGGGGGGATCAGCCCTCCAGGAAATGGT 60

.; 0 241 GTATTGCAATGGTGTCCTGGAGCCTCTGTACCTGTGCCCAAATGGTGCCCGCTGTGCCAC 300 241 GTATTICCALGOTGICCTGGAGCCTCTGTACCTGTGCCCAAATGGTGCCCGCTGTGCCAC 300 CTGGTTTCAAGACCCTACCCGCTTCACTGGCACCATGGATGCCTTCGTGAAGATCGTGAG 360 361 GCACGAGGGCACCAGGACCCTCTGGAGCGGCCTCCCCGCCACCCTGGTGATGACTGTGCC 420 61 Gecercadecaccogadereratracereterereterargaeaececeradacaeargada 120 180 180 240 CTGGTTTCAAGACCCTACCCGCTTCACTGGCACCATGGATGCCTTCGTGAAGATCGTGAG 360 1 croangerrenagaresersaceassacersesses resecces contransparas 60 GGTTCGCCTGCAGTCTCAGCGGCCCTCCATGGCCAGCGAGCTGATGCCTTCCTCCAGACT 121 Gerregeerigeagrereageggeericearggeeagegaagergargeerreereagaer GGCCTCAGGCACCGGGGCTGTGGTTACCTCTCTTCATGACACCCCTGGACGTGGTGAA GIGGAGCCICTACTACCAAATIGCCCTCCTCTCCAAICCACAGGGAAGIGCCTCCI 301 61 301 121 181 qq Q ò qq ò ò ò a ò q 8 g ò

ζ	421 AGCTACCGG	4.8	90
qu		AGCTACCGCCATCTACTTCACTGCCTATGACCAACTGAAGGCCTTCCTGTGTGGTCGAGC 480	90
Qy	481 CCTGACCTC	CCGT 54	0 #
qq	481 CCTGACCT	54	0 #
δy	541 GACTGTGAT	CITATGCGGACAAAGCTGCAGGCTCAGCATGTGTCGTA 60	00
qu	541 GACTGTGA	- P	00
ò	601 CCGGGAGC	CGAACTGCAGTGGCTCAGGGTGGCTGGGCGCTCACTGTG 66	0.0
qq	601 CCGGGAGC	9 9	9.0
δy	661 GCTGGGCT	CTGGGCTGGGGCCCACTGCCCTTCGAGATGTGCCCTTCTCAGCCCTGTACTGGTTCAA 720	2.0
qq	661 GCTGGGCT	72	20
δŏ	721 CTATGAGC	CTATGAGCTGGTGAAAGAGCTGGCTCAATGGGCTCAGGCCGAAGGACCAGACTTCTGTGGG 780	80
Op	721 CTATGAGC	78	80
70	781 CATGAGCT	84	0 4
qq	781 CATGAGCT	84	40
δλ	841 TGACGTGG	96	
쉽	841 TGACGTGG	90	
ò	901 CCCCCTGC	CCCCCTGCATGTGGACTCCACCTGGCTGCTGCGGAGGATCCGGGCCGAGTCGGGCAC 960	9
qa	901 CCCCCTGC	96	
ò	961 CAAGGGAC		
qq	961 CAAGGGAC	10	020
δλ	1021 CATGATCA	CATGATCAGCACCTATGACTTCGGCAAAGCTTCTTCCAGAGGCTGAACCAGGACCGGCT 108	
QC	1021 CATGATCA	10	
ò	180	TGGGGGCTGAAAGGGAAAGAAGAAC 1114	
QQ	1081 TCTGGGCG	GCTGAAAGGGGCAAGGACAAGGAC 1114	
REST AACT ID	LT 2 6992 AAC76992 standa	dard; cDNA; 1662 BP.	
AC AC	AAC76992;		
X 등 3	08-FEB-2001	(first entry)	
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Human ORFX ORF2547 polynucleotide sequence SEQ ID NO:5093.

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Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
XX
Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
XX
Human; open reading frame; osteopathic; antiatritic; immunosuppression;
XX
Humanstimalant; thrombolytic; coagulant; vasotropic; antidiabetic;
XX
Hypotensive; dermatological; immunosuppressive; antidiabetic;
XX
Humanaemic, gene therapy; cancer; proliferative disorder; hypertension;
XX
Humanemic, gene therapy; cancer; proliferative disorder; hypertension;
XX
Heurodegenerative disorder; osteoarthritis; graft vs host disease;
XX
Human of severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
XX
Holesterol ester storage; systemic lupus erythematosus; infection;
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Holesterol ester storage; systemic lupus erythematosus; infection;
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Holesterol ester storage; systemic lupus erythematosus; infection;
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Holesterol ester storage; systemic lupus erythematosus; infection;
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Holesterol ester storage; systemic lupus erythematosus; infection;
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Holesterol ester storage;
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antirheumatiî, antiproliferative, cârdiant, vasotropic,
cerebroprotective, neuroprotective, antibacterial, opthalmological;
gastrointestinal; nephrotropic, gynaecological; vulnerary; thrombolytic,
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GTATTGCAATGGTGTCTTGGAGCCTCTGTACCTGTGCCCAAATGGTGCCCGCTGTGCCAC 422
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                                               CTGGTTTCAAGACCCTACCCGCTTCACTGGCACCATGGATGCCTTCGTGAAGATCGTGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vectors. The proteins and mucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autofimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antinflammatory disease; to enhance
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1070; DB 21; Length
Pred. No. 3.2e-253;
0; Mismatches 10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 5; Page 4281-4282; 5507pp; English.
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Best Local Similarity 97.5%;
Matches 1104; Conservative (
                                                                                                                                                                                                                                       99US-0127636.
99US-0127728.
                                                                                                                                                                                                                                                                                      30-MAR-2000; 2000US-0540763.
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   AGCTACCGCCATCTACTTCACTGCCTATGACCAACTGAAGGCCTTCCTGTGTGGTCGAGC
                                                         CCTGACCTCTGACCTCTACGCACCCATGGTGGCTGGCGCGCTGGCCCGCCTGGGCACCGT
                                                                                                               GACTGTGATCAGCCCCCTGGAGCTTATGCGGACAAAGCTGCAGGCTCAGCATGTGTCGTA
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therapy; cancer; wound; infectious disease; thrombosis; arthritis;
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Pred. No. 8.5e-250;
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                  infertility; ss.
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18-AUG-1999;
12-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anyonory Various Carley Cutness were isolated iron indea inversion and incention and cloning. Some diverged from the reviously known CGI-69 sequence in that they encoded an 6-amino version' isoform or CGI-69 (see AAI71019). The invention relates to a novel characterization of CGI-69 as a mitochondrial carrier proceeded by a Wéd, change, and were termed the 'long version' isoform or CGI-69 (See AAI71019). The invention relates to a novel characterization of CGI-69 as a mitochondrial carrier protein, the discovery of CGI-69 is a mitochondrial carrier alteration of the mitochondrial membrane potential through overexpression of carboxyl-FLAG-tagged CGI-69. CGI-69 (including splice variant) nucleic acids and proteins are useful for diagnosing and treating metabolic diseases in humans, including obesity, cachexia and diabetes. Evidence for an important function for CGI-69 in modifying mitochondrial membrane potential in brown adipose tissue (BAT) is presented. The mouse orthologue of CGI-69 is up-regulated in cold-treated BAT. CGI-69 may be involved in calipose tissue (BAT) is presented. The mouse orthologue of CGI-69 is up-regulated in cold-treated BAT. CGI-69 may be involved in calipose and treat specific perturbations in metabolic pathways. Altering the expression of CGI-69 through gene therapy provides a means of treating metabolic diseases, such as obesity or cachexia, or of increasing or decreasing body weight. Decreasing its activity can be used to treat obesity, tumours, cancers, viral infections and bacterial infections, while increasing its activity can be used to creat obesity, tumours, cancers, viral infections and bacterial infections (all claimed). Methods are also calamade for determining whether a compound up regulates or ameaning whether a compound up regulates or ameaning whether a compound up regulates or ameaning per compound to a general processing or a mutation in the CGI-69 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTATTGCAATGGTGTCCTGGAGCCTCTGTACCTGTGCCCAATGGTGCCCGCTGTGCCAC 380
                                                                                                                                                                                                                                                                                                                    CGI-69 polypeptides and polynucleotides useful for treating metabolic disorders including cachexia, obesity, diabetes and cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GGCCTCAGGCACCGGGGCTGTGCTTACCTCTTCTTCATGACACCCCTGGACGTGGTGAA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGAAGCTTCAAGATGGCTGACCAGGACCCTGCGGGCATCAGCCCCCTCCAGCAAATGGT 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          present sequence is that of CDNA encoding human CGI-69 (see 0570). Various CGI-69 clones were isolated from human liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1054.4; DB 24; Length 1546; Pred. No. 2.1e-249;
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                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 11-12; 107pp; English
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     22-JUN-2001; 2001WO-US20117.
                                                              22-JUN-2000; 2000US-213307P
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                                                                                                                   GENENTECH INC
CURAGEN CORP.
                                                                                                                                                                                                      Lewin D, Adams SH,
                                                                                                                                                                                                                                                               WPI; 2002-114569/15.
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                                                                                                                                                                                                                             Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    represent PCR primers for a mouse ischaemic condition related sequence,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 ACCTCTACGCACCCATGGTGGCTGGTGCCCTCGCCCGAATGAG--CCGTGACAGTTGTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       which are used in the exemplification of the present invention.
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                                                                                                                                                    Ishii Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence 704 BP; 132 A; 204 C; 209 G; 159 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 2.3e-106;
                                                                                                                                                    Takahashi Y, Nagata T,
                                                                                                               (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
                                                                                                                                                                                                                                                                                                                              Claim 2; Page 1679-1680; 2690pp; English.
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                                                                           2000JP-0145977
                                                                                                                                                      Asai S,
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                                                                           18-MAY-2000;
                                                                                                                                                      shikawa K,
22-NOV-2001
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The invention relates to 625 polynucleotides which have been derived from a variety of human tissue sources and which encode novel secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proceins, their complements and sequences that hybridise to them. Also included are a vector comprising the polynucleotide, a host cell transformed with the vector, the proteins encoded by the polynucleotides, antibodies that bind to the proteins and identification of modularors of the proteins or the expression of the polynucleotides.

The polynucleotides can be used as probes for the identification and isolation of full length cDNA and genomic DNA. The polynucleotides and proteins can also be used as nutritional supplements. The protein is useful in the treatment of various immune deficiencies and disorders such as viral infections, bacterial infections, fungal infections, autoimmune disorders (e.g. rheumatoid architis, multiple sclerosis, autoimmune thyroiditis and diabetes) and allergic reactions and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Six hundred and twenty five polynucleotides derived from a variety of human tissue sources which encode secreted proteins, useful for treating immune deficiencies and disorders such as autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bacterial infection, fungal infection, autoimmune disorder; burn, rhemmatoid arthritis; multiple sclerosis; autoimmune thyroidiis; diabetes, allengy, asthma, neurodegenerative disease, Crohn's disease, Alzheimer's disease, Parkinson's disease; liver fibrosis; tumour; coagulation disorder, haemophilia, inflammatory disorder, ulcer, tissue regeneration; wound healing; haematopoiesis; myeloid deficiency;
                                                            1031
                                                                                                                                        1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; ss; gene; secreted protein; immune deficiency; viral infection;
                                                                                                                                                                            629
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480 IGGACTCCACCTGGCTCCTGCTTCGCAGAATCCGGGGTGAATCTGGCACCAGGGGACTCT
                                                                                    TIGCAGGCTICCTCCCCAGGATCATCAAGGCTGCACCCTCCTGTGCCATCATGATCAGCA
                                                                                                                                    CCTATGAGTTCGGCAAAAGCTTCTTCCAGAGGCTGAACCAGGACCGGCTTCTGGGCGGCT
                                                                                                                                                                    CTTACGAGTTTGGCAAAAGCTTCTTCCAGAGGCTCAACCAGGAGCAGCACCTCTTGGCCGCT
                                                            TIGCAGGCTTCCTTCCTCGGATCATCAAGGCTGCCCCCTCCTGTGCCATCATGATCAGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                secreted protein, SEQ ID 504.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Agostino MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 269-270; 339pp; English.
                                                                                                                                                                                                                                                                                                                                                ABK34735 standard; cDNA; 2170 BP.
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                               neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's disease), liver fibrosis, coagulation disorders (e.g. haemophilia), inflammatory disorders (e.g. Crohn's disease) and tumours. They are als useful for tissue regeneration, for wound healing and in the treatment of burns, incisions and ulcers. The proteins are also useful for regulating haematopoidesis, for treating myeloid or lymphoid cell deficiencies. The present sequence is one of the 625 cDNA sequences encoding a secreted protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2170;
   (e.g. asthma). They are also useful for treating
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                                                                                                                                                                                                                                                                                                                                                                                Sequence 2170 BP; 407 A; 663 C; 636 G; 460 T; 4 other;
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Pred. No. 3.2e-106;
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                                                                                                                                                                                                                                                                                                                                 Apoptosis; mouse; cancer; autoimmune disease; viral infection;
                                                                                                                                                                                                                                                                                                      Murine apoptosis related DNA sequence #84.
                                                                                                                                                                                                           ABL01419 standard; DNA; 758
                                                                                                                                                                                                                                                                         (first entry)
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15-MAR-2002

ABL01419

DE10126344-A1.

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nucleic acid is associated with appticois. The sequences can be used in the diagnosis treatment and prevention of diseases associated with excessive or inadequate apoticois, including tumours, autoimmune diseases, viral infections, degradative diseases (Alzheimer's, Parkinson's and Huntington's diseases), repertusion injury, stroke and alcohol-induced injury to the liver, for identifying agents for treating these diseases, and to prepare transgenic animals in which expression of an apopticois related sequence is altered. These are useful for genetic and/or pharmacological investigations of apopticis and related diseases, including dilatory cardiomyopathy. The present sequence is one of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New apoptosis-associated nucleic acid sequences and polypeptides, useful for diagnosis, treatment and prevention of e.g. tumors and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'n
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                                                                                                                                                                                                                                                                                                                                                  Gewies A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40.3%; Score 448.4; DB 24;
B2.9%; Pred. No. 1.5e-100;
iive 0; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                  Cramer U,
                                                                                                                                                                                                                                                                   (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       including dilatory cardiomyopathy. The presenapoptosis related sequences of the invention.
                                                                                                                                                                                                                                                                                                                                          Braziulis E, Cı
lle H, Klein M;
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                                                                                                                                                                                                                                                                                                                                                                                  Gille H,
                                                                                                               30-MAY-2001; 2001DE-1026344.
                                                                                                                                                                                       2000DE-1034303
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                                                                                                                                                                                                                                                                                                                                                                                      Albayrak T,
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Best Local Simil
Matches 533; C
                                   24-JAN-2002
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                                                                                                                                                                                                                                                                                                                               vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; otrombolyvic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; antiviral; antibacterial; antifungal; antirheumatic; antihrhyroid; antinaemic; gene therapy; cancer; proliferative disorder; hypotrension; nucleaguerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; colesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; noctural haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
588 TIGACCTCTGACCTCTACGCACCCATGGTGGCTGNTGCCCTCGCCCGAATGGGCACCGTG 647
                                                                                                                                                                                                                                                                                                                    frame; ORFX; detection; cytostatic; hepatotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   frame X,
                               ACTGTGATCAGCCCCTGGAGCTTATGCGGACAAAGCTGCAGGCTCAGCATGTGTCGTAC
                                                          Novel nucleic acids and peptides derived from open reading useful for treating e.g. Cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease
                                                                                                                                                                                                                                                                                        Human ORFX ORF2246 polynucleotide sequence SEQ ID NO:4491.
                                                                                                                  CTGAGCTGGCTINCTCTGTT-AAGCTGCNGNGACTCAGGGTG 748
                                                                                            CGGGAGCTGGGTGCTGTGTTCGAACTGCAGTGGCTCAGGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Page 3671-3675; 5507pp; English.
                                                                                                                                                                                                    BP
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                                                                                                                                                                                                   AAC76691 standard; cDNA; 6712
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05-APR-1999;
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AAC76691/c
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                                 vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, coagulation; to inhibit thrombosis; and as a contraceptive.
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acids can be used to express ORFX proteins in gene therapy. The proteins and nucleic acids may be used to treat cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                              21.7%; Score 242.2; DB 21; Length 6712; 56.2%; Pred. No. 1.3e-49;
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contacting a biological sample from a patient with (IV), detecting the amount of polymocleotide hybridising to (IV) and comparing the amount to patient, whire the amount of polymocleotide hybridising to (IV) is detected preferably by polymerase chain reaction (PCR) (I) comprising specific for an ovarian tumour protein comprising contacting T cells specific for an ovarian tumour protein comprising contacting T cells with (III) or (III) is useful in design and preparation of ribozyme molecules for inhibiting expression of the tumour polypeptides and proteins in tumour cells, and to isolate a full length gene from a suitable library e.g., a tumour cDNA library using well known
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a composition (I) comprising: carriers and immunostimulants; and a polypeptide (II) of a ovarian tumour polypeptide encoded by a polymulecide (III) having a cDNA sequence (SI) from the 10912 nuclectide sequences as given in ABL77023 to ABL87934, (III) encoding (II) having a sequence (S2), a T cell population of (II), or antigen presenting cells that express (II). (I) has cytostatic activity. An oligonuclectide (IV) that hybridises to (S1) can be used for detecting ovarian cancer in a patient's biological sample prefereibly searum or ovarian tissue. The method comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Composition for therapy and diagnosis of ovarian cancer comprising polypeptide of a ovarian tumor polypeptide, polynucleotide encoding polypeptide, antibody specific to polypeptide or T cell expressing polypeptide -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 24; Length 453;
                                                                                                                                                                       Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.
                                                                                                                                   Human ovarian cancer related cDNA clone SEQ ID NO:4486.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence 453 BP; 74 A; 154 C; 128 G; 97 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 185.8; DB 2
Pred. No. 4.5e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID 4486; 489pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Jones R;
                   ABL81508 standard; cDNA; 453 BP.
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92.0%;
                                                                                                                                                                                                                                                                                                                          29-MAY-2001; 2001WO-US17756.
                                                                                                                                                                                                                                                                                                                                                              26-MAY-2000; 2000US-207484P.
                                                                                                                                                                                                                                                                                                                                                                                                                                        SL,
                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                          Harlocker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-122075/16.
                                                                                                                                                                                                                                                                                                                                                                                                    (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                WO200192581-A2
                                                                                                                                                                                                               Homo sapiens.
                                                                                             17-MAY-2002
                                                                                                                                                                                                                                                                                    06-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Algate PA,
                                                       ABL81508;
ABL81508
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The invention relates to methods for predicting toxic effects of compounds or the progression of these toxic effects by determining the global changes in gene expression in tissues or calls exposed to the toxin and comparing these to gene expression in unexposed tissues or calls. Also included are methods of predicting at least one toxic effect of a compound or progression in unexposed tissues or calls ample exposed to the compound of two papersons of a toxic effect of a compound, comprising detecting the level of expression in a tissue or call sample exposed to the compound of two or more genes is indicative of at least one toxic effect or progression of the genes is indicative of at least one toxic effect or progression of toxic response and predict callular pathways that a compound modulates the toxic response and predict callular pathways that a compound modulates in a call. The methods utilise a set of at least two probes (on a solid support in kit form), where each of the probes comprises a sequence that specifically hybridises to a gene listed in the specification, a computer specifically hybridises to a gene listed in the specification, a computer system computation at tissue or call sample exposed to a hepatotoxin of a
                                                                                                                                                                                                                                                                                                                                       Rat sequence differentially expressed in response to a hepatotoxin #329.
                                     350 CGAACTGCAGTGGCTCAGGGTGGCTGGCCCTCACTGTGGCTGGGCTGGGC CCCACTGCC 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Predicting toxic effects of compounds or the progression of these tox effects by determining the changes in gene expression in tissues or cells exposed to the toxin and comparing these to gene expression in
                                                                                                                                                                                                                                                                                                                                                                            Rat; ss; hepatotoxin; expressed sequence tag; EST; drug screening; differential expression; centrilobular necrosis; steatosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Elashoff MR;
                                                                            683 CTTCGAGATGTGCCCTTCTCAGCCCTGTACTGGTTCAACTATGAG 727
                                                                                                                 409 circcadarcrecerrereacecretacrecircacrarcae 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Castle AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Seg ID No 329; 239pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Johnson KR,
                                                                                                                                                                                                                 ABK62422 standard; cDNA; 512 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-244880P.
2001US-290029P.
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2001US-292336P.
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2001US-297457P.
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19-JUN-2001; 2001US-298884P.
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                                                                                                                                                                                                                                                                                              18-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Porter MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GENE-) GENE LOGIC INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-241625/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200210453-A2.
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22-MAY-2001;
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                                                                                                                                                                                                                                                           ABK62422;
                                                                                                                                                                              RESULT 10
ABK62422/c
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17; Indels

0; Mismatches

Matches 207; Conservative

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Similarity

Local

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set of genes comprising at least two genes listed in the specification, and a user interface to view the information used to present information identifying the expression level in a tissue or cell of at least one gene listed in the specification. The method is useful for elucidating global
                                                                                                                           gene expression information may be used as diagnostic markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound or agent. Heparotoxicity is characterised by centrilobular necrosis and steatosis. The present sequence is an expressed sequence tag (EST) or CDNA derived from a gene which is differentially expressed in response to a hepatotoxic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGCTTCCTTCCTCGGATCATCAAGGCTGCCCCCTCCTGTGCCATCATGATCAGCACCTAT 1036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:387.
                                                                         changes in gene expression and for identifying toxicity markers in tissues or cell exposed to a known toxin. The genes may be used as toxicity markers in drug screening and toxicity assays. The genes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTTTCCTCCNCAGGATCATCAAGGCTGCGCCCTCCTGCGCCATCATCAGCACTTAC 332
                                                                                                                                                                                                                                                                                                                                                                                                          511 CAGCGACAAATGTCACTGGGAGCAGTGGAGGCTATGAGAGTGAAGCCGCCAAGAGTTGAC 452
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                                                                                                                                                                                                                                                                                                                                                                      CAACGCCAGGTCGCTCTGGGAGCGATGGAGGCTGTGAGGAGTGAACCCCCTGCATGTGGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                               917 TCCACCTGGCTGCTGCTGCTGCGGAGATCCGGGCCGAGTCGGGCACCCAAGGGACTCTTTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAGTTCGGCAAAAGCTTCTTCCAGAGGCTGAACCAGGACCGGCTTCTGGGCGGCTGAAAG
                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                DB 24; Length 512;
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Pred. No. 3.1e-32;
0; Mismatches 44; Indels
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                                                                                                                                                                                                                                                            Sequence 512 BP; 119 A; 129 C; 147 G; 116 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xu J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunogenic; cytostatic; vaccine; ss.
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                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                                            15.3%;
larity 81.7%;
Conservative (
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98US-0159812.
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                                                                                                                                                                                                                                                                                                                  Similarity
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09-APR-1999;
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                                                                                                                                                                                                                                                                                                                     Local Sim
es 196;
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polynuclectides encoding them, antigen presenting cells which express the polypeptides and vaccines comprising them can be used for inhibiting the development of prostate cancer in a patient. The polypeptides can be used to generate antibodies or anti-idiotypic antibodies for passive immuno therapy. A portion of the polynuclate the expression of the polypeptides can be used as a probe or Lo modulate the expression of the polypeptides. AAMOGA1 to AAMOGO1 and AAM32000 to AAW32020 represent sequences used in the exemplification of
                                                                                                                        The present invention describes isolated polypeptides, comprising an immunogenic portion of a prostate tumour protein (PTP). The polypeptides and polynucleotides encoding them have cytostatic activity and can be used in vaccines and in gene therapy. The polypeptides and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1064
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Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 ccccrccrcrcrcrcrcargarcagcaccrargarrcagcaaaagcrrcrrccagaggc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1005 CCCCCTCCTGTGCCATCATGATCAGCACCTATGAGTTCGGCAAAAGCTTCTTCCAGAGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 TGAACCAGGACCGGCTTCTGGGCGGCTGAAAGGGGCCAAGGACCAAGGAC 170
comprises an immunogenic portion of prostate tumor protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 537 BP; 116 A; 167 C; 138 G; 116 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 15.3%; Score 170; DB 21;
Best Local Similarity 100.0%; Pred. No. 3.6e-32;
Matches 170; Conservative 0; Mismatches 0;
                                                            Page 235-236; 263pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence #357.
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2000US-0636215.
2000US-0651236.
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2000US-0570737.
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2000US-0685166.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the present invention.
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12-MAY-2000;
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                                                               Claim 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAS63815;
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present invention describes polynucleotide sequences (I) which encode
                                                                                                                                                                                           prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I), (II), and can be used in vaccine production and gene therapy. (I), (II), (II), fusion proteins comparising (II), and isolated (II), and isolated (II) are used treat cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. The cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used for monitoring the progression of cancer in a patient. (I) and (II) can also be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastesis as well as the prostate volume. Ad#93357 to Ad#93944 and AAM0115 to AAM01318 represent polynucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1005 CCCCCTCCTGTGCCATCATGATCAGCACCTATGAGTTCGGCAAAAGCTTCTTCCAGAGGC 1064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 CCCCTCTGTGCCATCATCAGCACCTATGAGTTCGGCAAAAGCTTCTTCCAGAGGC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reed SG;
Wang A;
monitoring and treating prostate cancer in a patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1065 TGAACCAGGACCGGCTTCTGGGCGGCTGAAGGGGCCAAGGAGGAGGAC 1114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; prostate cancer; therapy; diagnosis; cat eye syndrome chromosome 22411.2; prostate-specific protein; chromosome 1; prostate specific antigen; PSA; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.3%; Score 170; DB 22; Length 537;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 TGAACCAGGACCGGCTTCTGGGCGGCTGAAAGGGGCAAGGAGCAAGGAC 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Harlocker SL, Jiang Y,
Day CH, Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 537 BP; 116 A; 167 C; 138 G; 116 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No. 3.6e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human prostate-specific cDNA sequence CGI-69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.0%; Pred. No. 3.6
Matches 170; Conservative 0; Mismatches
                                                                                               Claim 1; Page 359-360; 543pp; English.
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Kalos MD, Retter MW, Stolk JA,
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99US-0443686.
diagnosing, monitori
for use in vaccines
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                                                                                                                                                                                                                                                                                           polynuclectides, polypeptides, fusion proceins of the polypeptides, antibodies rated against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting calls expressing the polypeptides for antigenic epitopes polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting calls are useful for stimulating and/or expanding T calls specific for a tumour protein, and for inhibiting the development of cancer especially prostate cancer. Compositions composition the polynucleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The oligonucleotide is useful for
                                                                                        New human prostate-specific polypeptides and polynucleotides useful for the diagnosis and treatment of cancer, especially prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1005 CCCCCTCCTGTGCCATCATGATGAGCACCTATGAGTTCGGCAAAAGCTTCTTCCAGAGGC 1064
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YAW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 CCCCCTCTGTGCCATCATGATCAGCACCTATGAGTTCGGCAAAAGCTTCTTCCAGAGGC
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Retter MW, Stolk JA, Skeiky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is a prostate specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 170; DB 22; Length 537;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotide encoding a prostate-specific protein, for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 537 BP; 116 A; 167 C; 138 G; 116 T; 0 other;
                                                                                                                                                                                                                                                           The invention relates to isolated prostate-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Pred. No. 3.6e-32; ive 0; Mismatches 0;
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                                                                                                                                                                                               Claim 1; Page 361; 579pp; English.
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GR, Day CH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.3%;
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es 170; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               detecting cancer. The olynucleotide of the
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Wang A, Meagher MJ;
                            WPI; 2001-639232/73.
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MD, Fanger
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The present invention describes an isolated polypeptide (P1) comprising at least an immunogenic portion of a prostate-specific protein, or its variant. Also described are polymolectides (N1) encoding (P1). (P1) and (N1) have cytostatic activity and can be used in vaccine production. The polypeptides, nucleic acids and antibodies from the present invention are useful in the diagnosis and therapy of prostate cancer. Prostate specific genes P704p, P12p, P74pp, P75p and B305D are located in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome chromosome 1. AAH84671 to AAH85143 and AAG39000 to AAG39077 represent polymolectide and polypeptide sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                        Claim 31; Page 259; 325pp; English
prostate cancer
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Sequence 537 BP; 116 A; 167 C; 138 G; 116 T; 0 other;

Gaps 0; Ouery March 15.3%; Score 170; DB 22; Length 537; Best Local Similarity 100.0%; Pred. No. 3.6e-32; Matches 170; Conservative 0; Mismatches 0; Indels 0

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1005 CCCCCTCTGTGCCATCATGATCAGCACCTATGAGTTCGGCAAAAGCTTCTTCCAGAGGC 1064 op. ò ò

61 CCCCCTCCTGTGCCATCATGATCAGCACCTATGAGTTCGGCAAAAGCTTCTTCCAGAGGC 120 1065 TGAACCAGGACCGGCTTCTGGGCGGCTGAAAGGGGCAAGGAGCAAGGAC 1114 TGAACCAGGACCGGCTTCTGGGCGGCTGAAAGGGGCAAGGAGGCAAGGAC 170 121 ò qq g

AAH02787 standard; cDNA; 537 BP. 14-JUN-2001 AAH02787; RESULT 15 AAH02787

tumour antigen; prostate tumour; therapy; diagnosis; immunogenic; cytostatic; vaccine; ss. Prostate tumour antigen cDNA sequence for CGI-69. (first entry) Human; prostate t prostate cancer; 

WO200125272-A2

Homo sapiens

04-4 CT-2000; 2000WO-US27464.

99US-0157455 04-00T-1999;

(CORI-) CORIXA CORP.

WPI; 2001-245062/25.

Xu J, Skeiky YAW, Reed SG,

Cheever MA;

Prostate specific protein and its encoding polynucleotide, useful for the treatment and diagnosis of prostate cancer -Claim 50; Page 244; 276pp; English. The present invention describes an isolated polypeptide (1) comprising at least an immunogenic portion of a prostate tumour antigen protein or its variant. (1) have cytostatic activity and can be used in vaccine

ö production. (I), prostate tumour antigen polynucleotides, an antigen presenting call (AFC e.g. a dendritic cell) that expresses (I), and a pharmaceutical composition containing (I) are useful for inhibiting the development of cancer in a patient. Antibodies specific for prostate specific proteins and oligonucleotides that hybridise to a polynucleotide that encodes a prostate specific protein are useful for detecting the presence or absence of a cancer or monitoring the progression the progression of a cancer, especially prostate cancer. ANHOWAL2 to ANHORAYS to ANHOWAND and ANHOWAND are sequences used in the exemplification of the present invention. 1005 CCCCCTCCTGTGCCATCATGATCAGCACCTATGAGTTCGGCAAAAGCTTCTTCCAGAGGC 1064 61 coccrecrererearcarcaccaccrargacricegeaaaaccrrcracaaagc 120 Gaps 0 15.3%; Score 170; DB 22; Length 537; 100.0%; Pred. No. 3.6e-32; cive 0; Mismatches 0; Indels ( 121 TGAACCAGGACCGGCTTCTGGGCGGCTGAAAGGGGCAAGGAGGACGAAGGAC 170 Sequence 537 BP; 116 A; 167 C; 138 G; 116 T; 0 other; Search completed: January 22, 2003, 19:03:32 Job time : 280.466 secs Best Local Similarity 100.8 Matches 170; Conservative Query Match 1065 8888888888888 ò g g ð ò

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Issued Patents NA:\*

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

H	Sequence 68, Appl Sequence 68, Appl Sequence 387, App Sequence 23, Appl Sequence 23, Appl Sequence 24, Appl Sequence 14, Appl Sequence 61, Appl Sequence 61, Appl Sequence 61, Appl Sequence 61, Appl Sequence 6, Appli Sequence 6, Appli Sequence 31, Appl Sequence 31, Appl Sequence 11, Appli Sequence 13, Appli Sequence 11, Appli	/ 2 - 2 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -
SUMMARIES	US-08-933-750C-68 US-09-234-613-68 US-09-663-758-387 US-09-188-930-23 US-09-188-930-23 US-09-188-930-23 US-09-068-140A-14 US-09-068-140A-14 US-09-068-140A-14 US-09-234-613-61 US-08-931-750-61 US-08-91-871-11 US-08-91-871-11 US-08-91-91-91 US-08-91-91-91 US-08-16-218-11 US-08-16-218-11 US-08-16-218-11 US-08-16-218-11 US-08-234-332-3 US-09-234-332-3 US-09-385-028-15 US-09-385-028-13 US-09-385-028-13 US-09-385-028-13 US-09-385-028-13 US-09-385-028-13 US-09-385-028-13 US-09-385-028-13 US-09-385-028-13	
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0; Mismatches 1;
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APPLICANT: Guegler, Karl J.
APPLICANT: CORLEY, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                   TCTGGGCGGCTGAAAGGGGCAAGGAGCAAGGAC 1114
                                                                                                                         Incyte Pharmaceuticals, Inc
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APPLICATION NUMBER: US/08/933,750
FILING DATE: September 23, 1997
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US/09/234,613
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                                                                                                                                                                                                                           Sequence 68, Application US/09234613
Patent No. 6132973
GENERAL INFORMATION;
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Hillman, Jennifer L.
Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-055
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                            Shah, Purvi
Au-Young, Janice
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IBM Compatible
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TYPE: nucleic acid
STRANDEDNESS: single
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SEQUENCE CHARACTERISTICS:
LENGTH: 1643 base pairs
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CITY: Palo Alto
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CLASSIFICATION:
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                                             Score 1054.4; DB 2; Length 1643;
Pred. No. 3.9e-264;
); Mismatches 1; Indels 24;
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                                               94.6%;
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GGCCTCAGGCACCGGGGCTGTGGTTACCTCTTCTTCATGACACCCTGGACGTGAA 311
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RESULT 3

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APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
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APPLICANT: Xu, Jangchun
APPLICANT: Xu, Jangchun
APPLICANT: Witcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Harlocker, Susan Louise
APPLICANT: Rede, Seeven G.
APPLICANT: Ralos, Michael
APPLICANT: Refer, Mark
APPLICANT: Refer, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION DIAGNOSIS OF PROSTATE CANCER
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
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Best Local Similarity 100.0%; Pred. No. 4.3e-35;
Matches 170; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 210121.427C16
CURRENT APPLICATION NUMBER: US/09/605,785
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FastSEQ for Windows Version 3.0
                           Sequence 387, Application US/09605785
Patent No. 6321716
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Patent No. 6329505
GENERAL INFORMATION:
                                                                  GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Henderson, Robert A.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Follow, John A.
APPLICANT: Cariet, Marc W.
APPLICANT: Cariet, John A.
APPLICANT: Carter, Day, Craig H.
APPLICANT: Carter, Day, Craig H.
APPLICANT: Carter, Day, Chans S.
APPLICANT: Carter, Day, Chans S.
APPLICANT: Carter, Day, Chans S.
APPLICANT: Carter, Darrick
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US-09-605-785-387
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APPLICANT:
APPLICANT:
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                                                         Patent No.
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) ORGANISM: Mouse
US-09-188-930-262
                                                                                                                                                              ORGANISM: mouse
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US-09-188-930-262
                                                                                                                                                                     US-09-188-930-23
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LENGTH: 181
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                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                          Query Match
                                                                                                                                 LENGTH:
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                                                                                                                                                                                 CCCCTCCTGTGCCATCATGATCAGCACCTATGAGTTCGGCAAAAGCTTCCTGCAGAGGC
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APPLICANT: Harlocker, Susan Louise
APPLICANT: Harlocker, Vuqui
APPLICANT: Vu, Jiang, Yuqui
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Olandier Lynn
IIILE OF INVENTION: COMPOUNDS FOR IMMUNCTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
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100.0%; Pred. No. 4.3e-35;
iive 0; Mismatches 0;
                                                                                                   Score 170; DB 4; I Pred. No. 4.3e-35;
                                                                                        15.3%; Sco...
100.0%; Pred. No....
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0; Mismatches
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CURRENT APPLICATION NUMBER: US/09/352,616A
CURRENT FILING DATE: 1999-07-13
NUMBER OF SEQ ID NOS: 472
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SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 387
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 387, Application US/09352616A Patent No. 6395278 GENERAL INFORMATION:
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                                                                                                      Query Match
Best Local Similarity 100.C
Matches 170; Conservative
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Matches 170; Conservative
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                                           TYPE: DNA ORGANISM: Homo sapiens
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US-09-352-616A-387
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SEQ ID NO 387
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                                LENGTH:
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APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REPERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 23
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ilarity 52.1%; Pred. No. 1.2e-06;
Conservative 0; Mismatches 125;
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Pred. No. 9.4e-07;
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For Their Use
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CURRENT APPLICATION NUMBER: US/09/188,930A
UNRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
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Patent No. 6150502
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolate
TITLE OF INVENTION: and Methods For Thei
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Matches 136; Conservative
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Matches 136; Conserv
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/04807
FILING DATE: NO. 6281403ember 4, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Dinner, Dara L.
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; Sequence 14, Application US/09068140A
; Patent No. 6281409
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Dinner, Dara L.
REGISTRATION NUMBER: 33,680
REFERENCE/DOCKET NUMBER: C70
TELECOMMUNICATION INFORMATION:
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TELEFAX: 610-270-5090
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FILING DATE:
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433 CTACTTCACTGCCTATGACCAACTGAAGGCCTTCCTGTGTGGTCGAGCCCTGACCTCTGA 492
                   898 GATCCACGAAAGGCTTGTGGCAGGCTCCTTGGCCGGAGCCATTGCCCAGAGTAGCATCTA 957
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                                                               493 CCTCTACGCACCCATGGTGGCTGGCGCTGGCCCGCCTGGGCACCGTGACTGTGATCAG
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MEDLING TYPE: Floppy disk
COMPUTER: ISM PC comparatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/068,140A
FILING DATE:
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/04807
FILING DATE: No. 6201409ember 4, 1996
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 0.0015,
0; Mismatches 292; Indels
                                                                                                                                                                                                                                                                                                   APPLICANT: Mary Rose Woodhead, Mark Andrew Taylor PPLICANT: and Rex Michael Brennan. TITLE OF INVENTION: Blackcurrant Promoters and Genes CORRESPONDENCE ADDRESSE: ADDRESSE: SmithKline Beecham Corporation STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                    Sequence 9, Application US/09068140A Patent No. 6281409 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 33,680
REFERENCE/DOCKET NUMBER: C702:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                   CCCCTGGAGCTTATGCGGAC 573
                                                                                                                                                                     CCCAATGGAGGTTCTGAAGAC 978
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STREET: 709 Swedeland
CITY: King of Prussia
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Best Local Similarity 45.7
Matches 253; Conservative
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EDNESS: unknown
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US-09-068-140A-9
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266 GACTITACCGTGGGGTTGGTGGAATGGGTCTGGTGCAGGACCAGCTCACGCAGTGTAIT 325
                                                                                                                                                                    326 İCTCCGTTTACGAGATGTGAAGGAGACTTTTTCTCATGGTGATCCGAGC---AATTCCG 382
                                                                                                                                                                                                                                        498 ACGCACCCATGGTGGCTGGCGCTGGCCCGCCTGGGCACCGTGACTGTGATCAGCCCCC 557
                                                                                                                                                                                                                                                                                                        383 GTĠĊĠĊAĊĠĊĊĠŤŦŦĊĠĠĠĠŦĠŦŤĊĠĊĠAĊĠŦĠĠĊĀĠĊĠĠĸĠĠŦĠĀŦŦĀĊĠĊĠA 442
                                                                                                                                                                                                                                                                                                                                                                                TCACTGCCTATGACCAACTGAAGGCCTTCCTGTGTGGTCGAGCCCTGACCTCTGACCTCT 497
                                                                                                                                                                                                                                                                                                                                                                                                                                             443 İGGALGİGGİĞAARCAGAĞĞIİĞÇAĞITGÇAĞAGCAGTCÇĞIAÇAAĞĞGTGİTĞITĞATİ 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        618 GIGTITGAACTGCAGTGGCTCAGGGTGGCTGGCGCTCACTGTGGCTGGGCTGGGCCCCCA 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        503 GCGTGAGGAGGGTGTTGGTAGAAGGGATTGGCGCATTTTACGCATCTTATCGAACAA 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         563 CTGTGGTCATGAATGCCCCGTTTACGGCCGTTCACTTCGCCACATATGAAGCCACGAAGA 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           683 CTGCTGGTGCTGCTGGTGGAGCTTTGGCTGCAGTAGTAACCACTCCACTAGATGTTGTCA 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     623 AAGGGTTGTTGGAGGTGTCGCCGGAGACTGCGAACGATGAGAATTTGTTAGTGCATGCTA 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         678 CTGCCCTTCGAGATGTGCCCTTCTCAGCCCTGTACTGGTTCAACTA1GAGCTGGTGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             738 GCTGGCTCAATGGGCTCAGGCCGAA-----GGACCAGACTTCTGTGGGGCATGAGCTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 19406-0939

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Mary Rose Woodhead, Mark Andrew Taylor APPLICANT: and Rex M chael Brennan TITLE OF INVENTION: Blackcurrant Promoters and Genes NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS: ADDRESSE: SmithKline Beecham Corporation STREET: 709 Swedeland Road
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us-09-888-358-1.rni

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252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3787 AAGGGTTGTTGGAGGTGTCGCCGGAGACTGCGAACGATGAGAATTTGTTAGTGCATGCTA 3846
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             738 GCTGGCTCAATGGGCTCAGGCCGAA-----GGACCAGACTTCTGTGGGCATGAGCTTTG 791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               498 ACGCACCCATGGTGGCTGGCGCGCTGGCCCCTGGGCACCGTGACTGTGATCAGCCCCC 557
                                                                                                                                                                                                                                                                                                                                                 318 CCCGCTTCACTGGCACCATGGATGCCTTCGTGAAGATCGTGAGGCACGAGGGCACCAGGA 377
                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                378 CCCTCTGGAGCGGCCTCCCCGCCACCCTGGTGATGACTGTGCCAGCTACCGCCATCTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                438 TCACTGCCTATGACGAACTGAAGGCCTTCCTGTGTGGTCGAGCCCTGACCTCTGACCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TEGAGCITATGCGGACAAAGCTGCAGGTCAGCATGTGTCGTACCGGGAGCTGGGTGCCT
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                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                               Score 48.8; DB 4; Length 5150;
Pred. No. 0.0024;
0; Mismatches 292; Indels 9
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; Saquence 14, Application US/08232463
; Parent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: PALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITTY: Alexandria
STATE: VA
                                                                                                       DNA (genomic)
                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 45.7%;
                 i: 5150 base pairs
nucleic acid
EDNESS: unknown
                                                                                                                                                              ORIGINAL SOURCE:
ORGANISM: Ribes nigrum
STRAIN: Ben Alder
                                                                                                                                                                                                                                                                                                          Matches 253; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3907 AAACTCAGTTGCAG 3920
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGACCCAACGCCAG 865
                                                                             TOPOLOGY: unknown MOLECULE TYPE: DNA
                                                                                                                        8
                                                                                                                                             ANTI-SENSE: NO
                                                          STRANDEDNESS:
                                                                                                                      HYPOTHETICAL:
                                                                                                                                                                                                                           IS-09-068-140A-14
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                                                                                                                                                                                                                                                                   Query Match
                                        TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCAGGACCCTCTGGAGCGCCTCCCCCCCCCTGGTGATGACTGTGCCCAGCTACCGCCA 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132 AGICTCAGCGGCCCTCCATGGCCAGCGAGCTGATGCCTTCCTCCAGACTGTGGAGCCTCT 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             192 CCTATACCAAATTGCCCTCCTCTCTCCAATCCACAGGGAAGTGCCTCCTGTATTGCAATG 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTGTCCTGGAGCCTCTGTACCTGTGCCCAAATGGTGCCCGCTGTGCCACCTGGTTTCAAG 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 7218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 5.0%; Pred. No. 0.0055;
Matches 20; Conservative 213; Mismatches 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         492 ACCICIACGCACCCAIGGIGGCIGGCGCGCCGCCCCT
                                                                                                                                                                                                                                                                                                                                                        30472/114 IMMU
                                                                                                                                                                                                                                     FILING DATE: APPLICATION NUMBER: EP 91 114 300.6
                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 61, Application US/08933750C
Patent No. 592442
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
                                                                                                                                                                                                                                                                                                                                      29,768
                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)834-4109
                                                                                                                                                                                                                                                                            FILING DATE: 26-AUG-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 899149
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                 NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
ZIP: 22313-0299
COMPUTER READABLE FORM:
                                                                                                                                                                              CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pTZgpt-F1s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                           FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
US-08-933-750C-61
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TITLE OF INVENTION: HUMAN REGULATORY MOLECULES NUMBER OF SEQUENCES: 98 CORRESPONDENCE ADDRESS: ADDRESSES: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,613
                                                              Incyte Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE DOCKET NUMBER: PP-0356 US
IELECOMMUNICATION: INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750
FILING DATE: September 23, 1997
ATTORNEY/AGENT INFORMATION:
                                                                              STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 1594 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                              MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 415-845-4166
                                                                                                                                                     ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LIBRARY: SPLNNOT02; CLONE: 207452
US-09-234-613-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                            CA
USA
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IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                        FILING DATE
                                                                                                                                         COUNTRY:
                                                                                                                    STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1001 AGGAAGGCGCCTGGGCTTCTTCAAGGCCTGTCCCCCAGCTGCTGAAGGCTGCCTCT 1060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qy 1011 CCTGTGCCATCATGATCAGCACTATGAGTTCGGCAAAAGCTTCTTCCAGAGGCTGAAC 1069
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Pred. No. 0.082;
0; Mismatches 48; Indels 0,
                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOGTWARE: FastSEQ for Windows Version 2.0
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750C
FILING DATE: September 23, 1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                      APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: COTIEY, Neil C.
APPLICANT: COTIEY, Neil C.
NUMBER OF SEQUENCES: 96
                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INPORMATION:
NAME: Billings, Lucy J.
REGIGTRATION NUMBER: 36,749
REFERENCE/DOKET NUMBER: PF-0356 US
TELECOMMUNICATION INPORMATION:
TELEPHONE: 415-85-0555
Hillman, Jennifer L.
Bandman, Olga
Shah, Purvi
Au-Young, Janice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lal, Preeti
Hilman, Jennifer L.
Bandman, Olga
Shah, Purvi
Au-Young, Janice
Yue, Henry
Guegler, Karl J.
Corley, Neil C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 61, Application US/09234613
Patent No. 6132973
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.8%;
59.7%;
                                                                                                                                                                                                      3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1594 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71; Conservative
                                                                                                                                                                                                                                                                           ZIP: 94304
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIBRARY: SPLNNOT02
CLONE: 207452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             t Local Similarity
                                                                                                                                                                                                                            Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                  ADDRESSEE:
STREET: 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-933-750C-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                   APPLICANT:
APPLICANT:
APPLICANT;
                                                                                                                                                                                                                                                                 COUNTRY:
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APPLICANT:
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STATE:
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951 AGTCGGGCACCAAGGGACTCTTTGCAGGCTTCCTTCGGATCATCAAGGCTGCCCCCT 1010
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                                                                                                                                                                                                                                                                              us-08-961-871-11
; Sequence 11, Application US/08961871
; Patent No. 6013858
; Garran No. 6013858
; Garran No. 6013858
; Garran No. 6013858
; APPLICANT: Wallace, Douglas C.
APPLICANT: MacGregor, Grant R.
TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine
TITLE OF INVENTION: Nucleotide Translocator Protein and Methods
; TITLE OF INVENTION: Nucleotide Translocator Protein and Methods
; CORRESPONDENCE ADDRESS:
; STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STRATE: Colorado
COUNTRY: US
                                                                                                                                                                                                                                     1011 CCTGTGCCATCATGATCAGCACCTATGAGTTCGGCAAAAGCTTCTTCCAGAGGCTGAAC 1069
                                                                                                                                                                                                                                                                                          1061 CCACAGGCTTCATCTTCTTCTAGAATTCTTCTGTAATGTCTTCCACTGCATGAAC 1119
Query Match 3.8%; Score 42.2; DB 3; Length 1594; Best Local Similarity 59.7%; Pred. No. 0.082; Matches 71; Conservative 0; Mismatches 48; Indels 0.
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Patent No. 630377

GENERAL INFORMATION:
APPLICANT: Beclach C., Melanie
APPLICANT: McDaniel, Robert
TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES AND RECOMBINANT DNA
TITLE OF INVENTION: CONSTRUCTS THEREFOR
FILE REFERENCE: 30062-20030.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 443 GCCTATGACCAACTGAAGGCCTTCCTGTGTGGTCGAGCCCTGAGGCCTCTAGGCAC
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                                                                                                                                                             3.6%; Score 39.8; DB 4; Length 1192;
46.8%; Pred. No. 0.31;
tive 0; Mismatches 217; Indels 6
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                                                                                                                                                                                                     Best Local Similarity 46.8
Matches 196; Conservative
                                            ; ORGANISM: HOMO SAPIEN
US-09-142-565-1
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Best Local Simi
Matches 120;
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SEQ ID NO 6
                                                                                                                                                                         Query Match
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,871
ELING DATE: 31-OCT-1997
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 102;
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TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFREENCE: GH-30002
CURRENT APPLICATION NUMBER: US/09/142,565A
CURRENT FILING DATE: 1999-06-30
EARLIER APPLICATION NUMBER: 9704551.2
EARLIER PILING DATE: 1997-03-05
EARLIER FILING DATE: 1997-03-05
EARLIER FILING DATE: 1997-03-18
EARLIER FILING DATE: 1997-03-18
EARLIER FILING DATE: 1997-03-18
EARLIER FILING DATE: 1997-03-18
EARLIER FILING DATE: 1997-07-16
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                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NOBER: US 60/030.017
FILING DATE: 01-NOV-1996
ATTORNEY/AGENT INFORMATION:
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Patent No. 6187560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33,878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 78.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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E: DNA (genomic)
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APPLICANT: Lee James Beeley
APPLICANT: Kelly Paine
                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Ferber, Donna M. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 50.0
Matches 102; Conservative
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LOCATION:
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<sup>535</sup> GCCGCGCTCCACCT 548 g G

Search completed: January 22, 2003, 19:05:41 Job time : 75.6489 secs

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Sequence 2, Appli
Sequence 4486, Appl
Sequence 329, Appl
Sequence 387, Appl
Sequence 387, Appl
Sequence 387, Appl
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Sequence 46, Appl
Sequence 187, Appl
Sequence 1137, Appl
Sequence 1137, Appl
Sequence 1137, Appl
Sequence 1134, Appl
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                                                                                                                                                               January 22, 2003, 17:33:27 ; Search time 55.7 Seconds
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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCO7_NEW_PUB.seq:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-96-113-387

US-09-96-113-387

US-09-96-111674

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Listing first 45 summaries
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28253, A
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US-09-990-736-288
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## ALIGNMENTS

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	; SOUTWAKE: Patent ; SEQ ID NO 2 ; LENGTH: 1546 ; TYPE: DNA		Bess Matr		Qy 61 GGCCTCAGG	ବୁଣ ଦି	Db 225 GGTTCGCCT	0y 181 GTGGAGCCT	Qy 241	Db 321	- A	Qy 361	Db 441	- S	60 Qy 481 CCTGACC	Db 561	δ	1080 Db 621 GACTGTGAT 1080 Qy 601 CCGGGGAGCT	Db 681 CCGGGAGG	Qy 661 GCTGGGCTG	Db 741 GCTGGG	Oy 721 CTATGAGCT	801	0y /81 CATGAGCTT Db 861 CATGAGCTT	841		
241 GTATTGCAATGGTCTCTGGAGCCTCTGTACCTGTGCCCAATGGTGCCCGCTGTGCCAC 300	301 CTGGTTTCAAGACCCTACCGGCTTCACTGGCACCATGGATGCCTTCGTGAAGATCGTGAG 360 CTGGTTTCAAGACCCTACCGCACCATGGATGGATGCCTTCGTGAAGATCGTGAG 360	361 GCACGAGGGCACCACAGGACCCTCGGGGCCTCCCGGCCACCCTGGTGATGACTGTGCC 420	421 AGCTACCGCCATCTACTTCACTGCCTATGACCAACTGAAGGCCTTCCTGTGTGGTCGAGC 480	CCTGACCTCTGACCTCTACGCACCCATGGTGGCTGGCGGGCG	481 CCTGACCTCTGACCTCTACGCACCCGATGGCTGGCGGCGCGCCCCCCCTGGGCACCGT 540	541 GACTGTGATCAGCCCCTGGAGCTTATGCGGACAAAGCTGCAGGCTCAGCATGTGTCGTA 600 [	601 CCGGGAGCTGGCTGTGTTCGAACTGCAGTGGCTCAGGGTGGCTGGC	601 CCGGGAGCTGGCTGTCTTCGAACTGCAGTGGTTCAGGGTGGCTGGC	GCTGGGCTGGGGCCCCATGCCCTTCGAGATGTGCCCTTCTCAGCCCTGTACTGGTTCAA	121 CTATGAGCTGGTGAAGAGCTGGCTCAATGGGCTCAGGCCGAAGGACCAGACTTCTGTGGG 780	CATGAGCTTTGTGGCTGGTGGCATCTCAGGGACGGTGGCTGCAGACCAGACTTACCCTT		TGACGTGGTAAAGACCCAACGCCAGGTCGCTCTGGGAGCGATGGAGGCTGTGAGAGTGAA	TGACGTGGTAAAGACCCAACGCCAGGTCGCTCTGGGAGCGATGGAGGCTGTGAGAGTGAA 9	901 CCCCTGCATGTGGACTCCACCTGGTTGCTGCTGCGGAGAALCCGGGCCGAGTTGGGCAC 98	CAAGGGACTCTTTGCAGGCTTCCTTCCTCGGATCATCAAGGCTGCCCCTCCTGTGCCAT 1	CAAGGGACTCTTTGCAGGCTTCCTTCCTCGGATCATCAAGGCTGCCCCCTCCTGTGCCAT	CATGATCAGCACCTATGAGTTCGGCAAAAGCTTCTTCCAGAGGCTGAACCAGGACGGGCT	1 TCTGGGCGCTGAAAGGGCAAGGAC 1114	[		8-358-2 ce 2, Application US/09888358	NO. USŽČOZOI19137A1 L INFORMATION:	; APPLICANT: LEWIN, DAVID ; APPLICANT: ADAMS, SEAN H. APPLICANT: VI YING YING	OF INVENTION: CGI-69 COMPOSITIONS AND METHODS OF USE REFERENCE: 10716/66	NT APPLICATION NUMBER: US/09/888,358 NT FILING DATE: 2001-06-22	
Oy 2 Db 2	Oy 3	Oy 3 Db 3	4 4		Db 4	Oy 5	o <sub>y</sub> 6	9 9		7 7 7					S QQ			Oy 1021 Db 1021	Qy 1081	Db 1081	DECITE T	US-09-8	; Pater	; APPI	TITE	CURE	

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                                                                                                                                94.6%; Score 1054.4; DB 10; Length 1546; arity 97.8%; Pred. No. 4.9e-270; Onservative 0; Mismatches 1; Indels 24;
TION NUMBER: 60/213,307
DATE: 2000-06-22
ID NOS: 18
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CCCCCTGCATGTGGACTCCACCTGCTGCTGCGGAGGATCCGGGCCGAGTCGGGCAC
                                                                           CAAGGGACTCTTTGCAGGCTTCCTTCGTCGATCATCAAGGCTGCCCCCTCCTGTGCCAT
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                                                                                                                     1041 CAAGGGACTCTTTGCAGGCTTCCTTCGGATCATCAAGGCTGCCCCCTCCTGTGCCAT
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COMPUTER: IBM COMPARID: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: HUMAN REGULATORY MOLECULES NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                 TCTGGGCGGCTGAAAGGGGCAAGGAGGAC 1114
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FILING DATE: 23-Apr-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/518,865
FILING DATE: «UNKNOWN»
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ilbrary: Synooarol
CLONE: 724157
SEQUENCE DESCRIPTION: SEQ ID NO: 68
US-09-840-787-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lal, Preeti
Hillman, Jennifer L.
Bandman, Olga
Shah, Purvi
Au-Young, Janice
Yue, Henry
Guegler, Karl J.
Corley, Neil C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                         :ence 68, Application US/09840787
ent No. US20020058264Al
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1643 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 68: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <Unknown>
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STATE: CA
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US-^9-840-787-68
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94.6%; Score 1054.4; DB 10; Length 1643;

Query Match

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                 Gaps
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                                         CTGAAGCTTCAAGATGGCTGACCAGGACCCTGCGGGCATCAGCCCCCTCCAGCAAATGGT
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                Indels
 Pred. No. 5e-270;
0; Mismatches 1;
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 97.88;
Best Local Similarity 97.8
Matches 1089; Conservative
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Wang, Aijun
Skeiky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
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Mitcham, Jennifer L.
Harlocker, Susan L.
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Kalos, Michael D.
Retter, Marc W.
Stolk, John A.
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Vedvick, Thomas S.
Carter, Darrick
                                                                                                                                                                                                                                                                                                                                        ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 81.7
Matches 196; Conservative
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APPLICANT:
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1188 CATGATCAGCACCTATGAGTTCGGCAAAAGCTTCTTCCAGAGGCTGAACCAGGACCGGCT 1247
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                                                                                                                                                                                             Sequence 4486, Application US/09867701
; Sequence 4486, Application US/09867701
; GENERAL INFORMATION:
; APPLICANT: Aplate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF OVARIAN CANCER
; FILE REPRENCE: 2010.14.497
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTHARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4486
; LENTH: 453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     409 CTTCGAGATGTGCCTTCTCAGCCCTGTACTGGTTCAACTATGAG 453
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APPLICANT: Castle, Arthur
APPLICANT: Elashoff, Michael
APPLICANT: Gene Logic, Inc.
ITILE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 4921-5038-US
CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31
                                                  1081 TCTGGGCGGCTGAAAGGGGCAAGGAGGAC 1114
                                                                                                1248 reregecegereaaagegeaageaageaageac 1281
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PRIOR APPLICATION INVIBER: US 60/222,040
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR FILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR FILING DATE: 2001-05-11
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PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: US 60/292,336
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Sequence 329, Application US/09917800A
Patent No. US20020119462A1
GENERAL INPORMATION:
APPLICANT: Mendrick, Donna
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ORGANISM: Homo sapien
                                                                                                                                                                                                US-09-867-701-4486
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977 GGCTTCCTTCCTCGGATCATCAAGGCTGCCCCTCCTGTGCCATCATGATCAGCACCTAT 1036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTHER INFORMATION: Genbank Accession No. US20020119462Al AA926365
NAME/KEY: misc feature
LOCATION: (1)...(512)
CTHER INFORMATION: n = a or c or g or t
US-09-917-800A-329
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APPLICANT: Wantenabe, Yoshihiro
APPLICANT: Meagher, Madeline Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.3%; Score 170.2; DB 10; Length 512; 81.7%; Pred. No. 6.1e-36; ive 0; Mismatches 44; Indels 0;
PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/295,798
PRIOR FILING DATE: 2001-06-06
PRIOR PLICATION NUMBER: US 60/297,457
PRIOR PLICATION NUMBER: US 60/297,457
PRIOR PLICATION NUMBER: US 60/296,884
PRIOR PLICATION NUMBER: US 60/303,459
PRIOR FILING DATE: 2001-06-19
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 1740
SOFTWARE: PATENTIN VOR: 1740
SEQ ID NO 329
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Indels
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Pred. No. 7.1e-36;
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100.0%; Pred. No. '...
'' Mismatches
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Houghton, Raymond L.
Virals de Bassols, Carlota
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Publication No. US20020193296Al
GENERAL INFORMATION:
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Jiang, Yudiu
Kalos, Michael D.
Retter, Marc W.
Stolk, John A.
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
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Henderson, Robert A.
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Vedvick, Thomas S.
Carter, Darrick
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ORGANISM: Homo sapiens
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Best Local Similarity
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US-09-759-143-387
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
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                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                           Query Match 15.3%; Score 170; DB 9; L
Best Local Similarity 100.0%; Pred. No. 7.1e-36;
Matches 170; Conservative 0; Mismatches 0;
DIAGNOSIS OF PROSTATE CANCER
             FILE REFERENCE: 210121.427C27
CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SEQ ID NO 387
LENGTH: 537
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CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: PastSEQ for Windows Version 3.0
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McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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US-09-995-72,
Sequence 387, App.
Publication No. US200201.
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
'POPLICANT: Dillon, Davin C.
'NOTLICANT: Mitcham, Jennifer L.
'Notlican', Jensen L.
'Notlican', Susan L.
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o. US20020192763A1
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Jiang, Yuqiu
Kalos, Michael D.
Retter, Marc W.
Stolk, John A.
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Hepler, William T.
Henderson, Robert A.
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Vedvick, Thomas S.
Carter, Darrick
Li, Samuel X.
                                                                                                                            TYPE: DNA
CORGANISM: Homo sapiens
US-10-012-896-387
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ORGANISM: Homo sapiens
TITLE OF INVENTION:
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
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CCCCCTCTGTGCCATCATGATCAGCACCTATGAGTTCGGCAAAAGCTTCTTCCAGAGGC 1064
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                                                         61 ccccrccrcrcrcrcarcarcacaccraraacrrcagcaaaaacrrcrrccagaggc 120
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APPLICANT: Foy, Teresa
APPLICANT: Eager, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427026
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                     1065 TGAACCAGGACCGGCTTCTGGGCGGCTGAAAGGGGGCAAGGAGGAGGAC 1114
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1005 CCCCTCCTGTGCCATCATCAGCACCTATGAGTTCGGCAAAAGCTTCTTCCAGAGGC 1064
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121-427024
CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSEQ for Windows Version 3.0
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 21012.153401
CURRENT PILING DATE: 2001.03.28
CURRENT FILING DATE: 2001.03.28
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 387
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 15.3%; Score 170; DB 10;
Best Local Similarity 100.0%; Pred. No. 7.1e-36;
Matches 170; Conservative 0; Mismatches 0;
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; Patent No. USZ00200045230A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
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Best Local Similarity 100.
Matches 170; Conservative
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7 TYPE: DNA
CRGANISM: Homo sapiens
US-09:780-669-387
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CRCANISM: Homo sapiens
US-09-822-827-387
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US-09-908-711-46
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 7.1e-36;
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y 100.0%; Pred. No. ..
... 0; Mismatches
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Patent No. US20020051977A1
                                                        Xu, Jiangchun
Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yugui
Henderson, Robert A.
Kalos, Michael D.
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
                                                                                                                                                                                                                                                          Fanger, Gary R.
Stelter, Marc W.
Stolk, John A.
Day, Craig H.
Odvick, Thomas S.
Carrer, Darrick
Li, Samuel
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McNeill, Patricia D.
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Hepler, William
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US20020022248A1
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Best Local Similarity
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GENERAL INFORMATION:
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THILE OF PAPELLANISM NAMES 1979-90,711

COMPARIATOR NAMES 1970-1104

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APPLICANT: Warren, wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John Wathialagan, Nagappan
TITLE OF INVENTION: WUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: WOSCIE AND FAT DEPOSITION
FILE REPERENCE: 16511.006/37-21(10298)c
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT APPLICATION NUMBER: 2001-09-24
SEQ ID NOS: 15112
SEQ ID NO 2543
LENGTH: 246
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                                                                                                                                                                                                                                                                                                                                                                 Length 275;
                                                                                                                                                                                                                                                                                                                                                               13.8%; Score 154; DB 10; Length 2
89.7%; Pred. No. 9.6e-32;
tive 2; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) ORGANISM: Bos taurus
) OTHER INFORMATION: Clone ID: 11-LiB34-070-Q1-E1-C11
US-09-960-352-2543
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                                                                                                                                                                                                                                         NAME/KEY: SITE
LOCATION: (246)
// OTHER INFORMATION: n equals a,t,g, or c
US-09-908-711-46
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Patent No. US20020137139A1
GENERAL INFORMATION:
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/209,467
PRIOR FILING DATE: 2000-06-07
WUMBER OF SEQ ID NOS: 167
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 89.79
Matches 174; Conservative
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                                                                                                                                                                     TYPE: DNA ORGANISM: Homo sapiens
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Best Local Similarity
Matches 138; Conserv
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                                                                                                                     SEQ ID NO 46
LENGTH: 275
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Search completed: January 22, 2003, 19:07:54 Job time : 70.7 secs
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Parent No. US202020489763A1

GRNERAL INFORMATION:
GRNERAL INFORMATION:
APPLICANT: Penn, Sharion G.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT PAPLICATION NUMBER: US/09/9864,761

CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 2000-02-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Genbank Accession No. US20020142981A1 AA450247
US-09-880-107-1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
           Sequence 1133, Application US/09880107

Patent No. US20020142981A1

GENERAL INFORMATION:

APPLICANT: Horne, Darci T.

APPLICANT: Scherf, Uwe

APPLICANT: Scherf, Uwe

TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer:

TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer:

TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer:

TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer:

TITLE REPERBRICE: 4921-5028-WO

CURRENT APPLICATION NUMBER: US 60/211,379

PRIOR FILING DATE: 2000-06-14

PRIOR FILING DATE: 2000-06-14

PRIOR FILING DATE: 2000-06-14

PRIOR FILING DATE: 2000-10-02

NUMBER OF SEQ ID NOS: 3950

SOFTWARE: PatentIN Ver. 2.1

SEQ ID NO 1133

LENGTH: 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.4%; Score 93.4; DB 10; Length 452; 98.9%; Pred. No. 1.3e-15; artive 0; Mismatches 1; Indels 0
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2001-01-30
PRIOR PRIOR DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR PRIOR DATE: 2001-01-30
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FILING DATE: 2001-01-30
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ORGANISM: Homo sapiens
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Best Local Similarity
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US-09-880-107-1133/c
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.97

OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 0.94

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.86

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 49117
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SEQ ID NO 11674
LENGTH: 452
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PELICATION NUMBER: PCT/US01/00661
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR PELING DATE: 2000-09-21
PRIOR PELING DATE: 2000-09-21
PRIOR PELING DATE: 2000-09-21
PRIOR PELING DATE: 2000-09-21
PRIOR PELING DATE: 2000-06-30
PRIOR PELING DATE: 2000-06-30
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Best Local Similarity 64.49
Matches 112; Conservative
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ORGANISM: Homo sapiens
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AK002381 Mus muscu BQ683596 AGENCOURT AK019396 Mus muscu BM923995 AGENCOURT

AL519987 BM459839 AL529906 BM468665

BI768227 BI759919 AL516722 AL528266 BM923251 BG470240

AL514846

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BM 5987 ALS 1987 ALS 1987 ALS 1998 AGEN COURT BM 6986 A AGEN COURT BM 6986 A AGEN COURT BM 6986 A AGEN COURT BM 5987 AGEN COURT BM 5987 AGEN COURT BM 5987 AGEN COURT BM 5988 AGEN COURT BM 5988 AGEN COURT BM 5988 AGEN COURT BM 5988 AGEN COURT BM 5988 AGEN COURT BM 5988 AGEN COURT BM 5988 AGEN COURT BM 5988 AGEN COURT BM 5988 AGEN COURT BM 5988 AGEN COURT AKO 10272 AUS MUSCURT AKO 1988 AGEN COURT AKO 1988 AGEN COURT AKO 1988 AGEN COURT AKO 1988 AGEN COURT AKO 1988 AGEN COURT AKO 1988 AGEN COURT BM 6978 AGEN COURT BM 64148 AGEN COURT BM 64148 AGEN COURT BM 64148 AGEN COURT BM 64148 AGEN COURT BM 64148 AGEN COURT BM 64148 AGEN COURT BM 5188 AGEN COURT BM 5188 AGEN COURT BM 5188 AGEN COURT BM 5188 AGEN COURT BM 518130 ALS 18130

BM915493 BQ949458 BQ934841 BG470248 BG688847 BQ071835 BQ071835 BK01072 BM8018978 ALS55763

BQ073154 AL547590 BG470228 AL545150

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BQ647782 BQ647042 BM464148 BM917004

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Functional prediction of the coding sequences of 79 new genes deduced by analysis of cDNA clones from human fetal liver Unpublished 2 (Dases I to 1402)
Zhang,C., Yu,Y., Zhang,S., Wei,H., Zhang,Y., Zhou,G., Bi,J., Liu,M. And Hef.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (13-JAN-1999) Department of Experimental Hematology, Institute of Radiation Medicine, Beijing Taiping Road 27, Beijing, Beijing 100550, P. R. China Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Zhang, C., Yu,Y., Zhang,S., Wei,H., Zhang,Y., Zhou,G., Bi,J., and He,F.
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Homo sapiens PRO2163 mRNA, complete cds.
AF119864
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(c) 1993 - 2003 Compugen Ltd.
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BM018915 BG749617 BM457688

Liu, M.

us-09-888-358-1.rst

892

952

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/cissue_type="medulla"
/lab_bost="DH10B"
/lab_bost="DH10B"
/note="Corgan: brain; Vector: pcWV-SPORTG; Site_1: Not!;
Site_2: ECGRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (ECGRV site is destroyed upon cloning)
/ Library is normalized and enriched for cloning anonymous male age 27. Library is destroyed upon cloning.
/ Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH MCC Library."
// Sa 327 c 302 g 213 t 3 others
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Email: cgapbs-remail.nin.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llhl.gov
Plate: LLAM12760 row: e column: 06
                                                                            CTACCCTTTGACGTGAAAGACCCAACGCCAGGTCGCTCTGGGAGCGATGGAGGCTGTG
                                                                                                                                                     AGAGTGAACCCCCTGCATGTGGACTCCACCTGGCTGCTGCGGGAAGGATCCGGGCCGAG
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Location/Qualifiers
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/clone="IMAGE:5742317"
/clone_lib="NIH_MGC_119"
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BM554056.1 GI:18793328
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Best Local Similarity 98.5
Matches 958; Conservative
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AK007934 1450 bp mRNA linear HTC 19-JAN-2002 Mus musculus 10 day old male pancreas CDNA, RIKEN full-length

RESULT 3 AK007934 LOCUS DEFINITION

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Arakawa, T., Haraya, R., Pukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I. Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gasterland, T., Gissi, C., King, B., Kochiwa, H., Kuchi, P., Leeris, S., Matsuo, Y., Nikaido, I., Pesole, G., Ouackenbush, J., Schriml, D., N., Staubli, F., Suzuki, R., Tomica, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blorefelli, D., Bojunga, N., Carninci, P. de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyo-oka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Washizaki, Y., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y.
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enriched library, clone:1810062G21:homolog to HYPOTHETICAL 38.5 KDA
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Nature 409 (6821), 685-690 (2001)
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High-efficiency full-length cDNA cloning
Meth. Fnzymol. 303, 19-44 (1999)
99279253
                              PROTEIN, full insert sequence.
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421 505 481 565 541

601 625

685 661 745

805 721

781 865 901

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AK007276 1371 bp mRNA linear HTC 19-JAN-2002 Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:1700125C18:homolog to HYPOTHETICAL 38.5 KDA PROTEIN,
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/db_xref="MGD:MG1:1915316"
/translation="MDDODPGGISPLQQMVASGAGAAVVISLFWIPLDVVKVRLQSQRP
                                                                                                                                               Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Gemomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Subhiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
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DVVKTQRQMSLGAVEAVRVKPPRVDSTWLLLRRIRAESGTRGLFAGFLPRIIKAAPSC
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RFTGTLDAFVKIVRHEGTRTLWSCLPATLVWTVPATAIYFTAYDQLKAFLCGQSLTSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse Lissues. First strand CDNA was primed with a primer
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/clone_lib="RIKEN full"length enriched mouse cDNA library"
/dev_stage="10 day old"
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                                                                                                                                                                                                                                                                                                                                                                                                        Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yamanaka,I.,
Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and
Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                  URL: http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
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Pred. No. 2.2e-195;
0; Mismatches 154;
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456 c 402 g 325
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/strain="C57BL/6J"
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Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RKEN), Laboratory for Genome Exploration Research Group, TKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp,
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WGPTALRDVPFSALYWENYELVKSWLSGLRPKDQTSVG1SFVAGG1SGMVAATLTLPP
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
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                                                                                                                                                                                                                                                                                                                   Please visit our web site (http://genome.gsc.riken.go.jp/) for
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85.6%; Pred. No. 2.5e-191;
live 0; Mismatches 157; Indels 1;
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/db_xref="PANTOM DB:1700125C18"

/db_xref="NGD:NGT:1896541"

/db_xref="taxon:10990"

/clone="1700125C18"
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/db_xref="G1:12840722"
/db_xref="MGD:MG1:1915316"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Toh, M., Komo, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length con 1 brazies for rapid discovery of new genes Genome, Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Korno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, B., Natahiki, M., Yoneda, Y., Ishikawa, T., Orawa, K., Tanaka, T., Matsuura, S., Kawai, J., Kazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-184-format Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                   Mus musculus (strain:C57BL/6J) adult male testis cDNA to mRNA, clone lib:RIKEN full-length enriched mouse cDNA library clone:1700125C18.

Mus musculus
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Location/Qualifiers
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length CONA libraries and normalization
Unpublished (2001)
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BP 191 91006 EVRY cedex - France
Email: segref@qenoscope.cns.fr. Web : www
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/tissue type="neuroblastoma cells"
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/lab_host="DH10B"
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was primed with a Nor1-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contect: Feng Liang Life
Technologies. a division of Invitrogen 9800 Medical Center
Brive Rockville, Maryland 20850, USA Pax: (1) 301 610
8371 Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com"
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Pred. No. 5.2e-190;
); Mismatches 0;
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/sex="male"
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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
1. oation/Qualifiers
1. oation/Qualifiers
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Li W.B., Gruber, C., Jessee, J. and Polayes, D.
Upublished to Malibraries and normalization
Contact: Genoscope
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/lab_host="neuroblastoma, cell line"
/lab_host="neuroblastoma, cell line"
/lab_host="neuroblastoma; site l: XhoI; site 2:
foote=""organ: brain; vector: poTBT; site 1: XhoI; site 2:
ECORI; cDNA made by oligo-dr priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >SONDb for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC Library."

2 others
                                                                                                                                         BQ883556 900 bp mRNA linear EST 16-AUG-2002 AGENCOURT 8727656 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:63408465', mRNA sequence.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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CATGAGCTTTGTGGCTGGTGGCATCTCAGGGACGGTGGCTGCAGTGCTGACTCTACCC 838
                     834 CATGAGCTITGTGGCTGGCGGTGCCATCTCAGGACGGTGCTGCAGTGCTGACTCTACCC 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA Library Preparation. Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Biosociance Corporation
Clone distribution: MGC clone distribution information can thutp://image.llnl.gov
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Pred. No. 5.2e-190;
0; Mismatches 21;
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/db xref="taxon:9606"
/clone="IMAGE:6340846"
/clone_lib="NIH MGC 47"
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Location/Qualifiers
1. .900
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Tissue Procurement: ATCC
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al Similarity 97.1%;
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894 TTTGACGTGGTAAAGACCMA 913

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enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCWNSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 8800 Medical Center Drive Rockville, Maryland 2086. USA Fax: (1) 301 610 8371 http://fulllength.invitrogen.com"
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al Similarity 98.5%;
847; Conservative 8
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Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunish, Y., Konno, H., Adachi, J., Fukuda, S., Aizwaa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashiburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gassrerland, T., Gissi, C., King, B., Kochiwa, H., Kuchl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomica, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blomstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Nordone, P., Ring, B., Ringyald, M., Raziya, M., Lee, N.H., Lyons, P., Nordone, P., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y.
                                                                             HTC 19-JAN-2002
                                                                   ik002381
iks musculus adult male kidney cDNA, RIKEN full-length enriched
ibrary, clone:0610009E11:homolog to HYPOTHETICAL 38.5 KDA PROTEIN,
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                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Nature 409 (6821), 685-690 (2001)
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Mus musculus (strain:C57BL/6J) adult male kidney cDNA tc
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clone:0610009E11.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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                                                                                                                                                                                                Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Vokohama Institute; 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-045, Japan (B-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp, Tel:81-45-503-9222,
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/doone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
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                                                                                                                                                                                                                                                                                                                 Please visit our web site (http://genome.gsc.riken.go.jp/) for
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/db_xref="FANTOM_DB:0610009E11"
/db_xref="MGD:MGI:1892017"
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85.7%; Pred. No. 1.2e
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoR1; cDNA made by oligo-d7 priming. Directionally cloned
                                                                                                                                                                                                                                                                                                                                                                                                               into EcoRI/XhoI sites using the following 5' adaptor: GGGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) Superscript IR T (Life Technologies). Note: this is a NIH_MGC Library."
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
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High-efficiency Full-length cDNA cloning
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (18-AUG-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tauruni-ku, Yokohama, Vanagawa 230-045, Japan (B-mail:genome-res@gsc.riken.go.jp, Fax:81-45-503-9216)
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                                            Length 1491;
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Matches 938;
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/organism="Mus musculus"

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/strain="C57BL/6J"

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/db\_xref="MGD:MGI:1915316"

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Search completed: January 23, 2003, 00:15:26
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/tissue_type="leiomyosarcoma"
/lab_host="MHIOB phage-resistant)"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
NA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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Pred. No. 5.9e-179;
); Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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/db_xref="taxon:9606"
/clone="IMAGE:5535960"
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Location/Qualifiers
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281
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         --GGAAGTGCCTCCT 221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   881
                                     241 GTATTGCAATGGTGTCCTGGAGCCTCTGTACCTGTGCCCAAATGGTGCCCGCTGTGCCAC
                                                                     222 GTATTGCAATGGTGTCCTGGAGCCTCTGTACCTGTGCCCAAATGGTGCCCGCGGTGCCAC
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186 GTGGAGCCTCTCCTATACCAAAT---
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